BEST AVAILABLE COPY

SEARCH REQUEST FORM

		hnical Information Center
Requester's Full Name: Art Unit: /(-5 3) Pho Mail Boy and Bldg/Room Log	My Schniz one Number 30	LY Examiner # : 7(55% Date: Serial Number: 09/44428/
	ation:	Results Format Preferred (circle): PAPER DISK E-MAI
If more than one search is si	uhmittad: nlass	ioritize searches in order of need. ***********************************
Include the elected species or structure	res, keywords, synonyms,	scribe as specifically as possible the subject matter to be searched, acronyms, and registry numbers, and combine with the concept or
Title of Invention:		·
Inventors (please provide full name	s):	
Earliest Priority Filing Date:		
appropriate serial number.	iciaue un periment informa	ttion (parent, child, divisional, or issued patent numbers) along with the
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ocher Shepponic	Type of Search	Vendors and cost where applicable
cher Phone #: 308-4494	NA Sequence (#)	STN
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Searcher Picked Up/	Bibliographic	Dr.Link
Searcher Picked Up/	Bibliographic	Dt.Link
e Searcher Picked Up/		
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Result
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Copyright (c) 1993 - 2003 Compu
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oxt chance 10-con-1999	RESULT 1 IC1222 Indolicidin precursor - bovine N;Alternate names: antimicrobial peptide N;Species: Bos primigenius taurus (cattle) N;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 N;Accession: JC1222: A42387: S5864	ne bia: buru	bovine imicrobi	cursor - es: antir primigen:	RESULT 1 IC1222 Indolicidin precursor NyAlternate names; an Species: Bos primig Jate: 10-Sep-1999 #	WESULT 1 IC122 IC122 IC122 IV Alternate names: an Valternate names: an Valternate names: an Valternate names: Total Name (Name 1999) INTERNATION (Name 1999) INTERNATION (Name 1999)
	ALIGNMENTS		٠			
hypothetical prote	T46458	N	278	50.0	43	45
probable cobalamin	A83506	N	250	50.0	43	44
arylesterase (EC 3	JQ0606	Ŋ	236		43	43
conserved hypothet	D72081	2	192	50.0	43	42
hypothetical prote	H86543	2	192		43	41
light-harvesting p	S23291	N	51		43	40
ATP-binding casset	A59189	Ν	1529		43.5	39
probable esterase	AH0244	ν	276		43.5	38
E2 glycoprotein pr	S14940	N	1162		44	37
E2 glycoprotein pr	S14939	2	1162		44	36
	S07421	2	1162	51.2	44	35
	VGIHAK	↦	1162		44	34
E2 glycoprotein pr	VGIHIB		1154		44	33
hypothetical prote	T00322	۵	968	1.	44	32
	F70746	ż	968	51.2	44	31
probable mmpL4 pro	C70831	2	967	51.2	44	30

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RESULT 1

JC1222

Indolicidin precursor - bovine
N;Alternate names: antimicrobial peptide
C;Species: Bos prinigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-199
C;Accession: JC122; A42387; S25664
R;del Sal, G; Storici, P; Schneider, C; Romeo, D; Zanetti, M.
Biochem. Biophys. Res. Commun. 187, 467-472, 1992
A;Title: cDNA cloning of the neutrophil bactericidal peptide indolicidin.
A;Reference number: JC1222; MUID:92392368; PMID:1520337
A;Rocession: JC1222
A;Molecule type: mRNA
A;Residues: 1-144 <SAL>
A;Resid
                                    E2 glycoprotein precursor - human coronavirus (strain 229E)
N;Alternate names: peplomer glycoprotein; S glycoprotein; spike glycoprotein
C;Species: human coronavirus
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Jun-2000
C;Accession: A34766; S05460
R;Raabe, T.; Schelle-Prinz, B.; Siddell, S.G.
                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 2
VGIHHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Experimental source: neutrophils
A;Note: sequence extracted from NCBI backbone (NCBID:83840)
C;Superfamily: cathelin; cystatin homology
C;Keywords: amidated carboxyl end
F;1-29/Domain: signal sequence #status predicted <SIG>F;22-129/Domain: cystatin homology <CYS>
F;30-30/Domain: propeptide #status predicted <PRO>
F;31-143/Product: indolicidin #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Experimental source: bone marrow R;Selsted, M.E.; Novotny, M.J.; Morris, W.L.; Tang, Y.Q.; Smith, W.; Cullor, J.S. J. Biol. Chem. 267, 4292-4295, 1992.
J. Biol. Chem. 267, 4292-4295, 1992.
A;Title: Indolicidin, a novel bactericidal tridecapeptide amide from neutrophils.
A;Reference number: A42387; MUID:92165771; PMID:1537821
A;Accession: A42387
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R; Raabe, T.; St
J. Gen. Virol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;143/Modified site: amidated carboxyl end (Arg) (amide in mature form from following
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Best Local :
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Schelle-Prinz, B.; Siddell, S.G
1. 71, 1065-1073, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
8; Conserv
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C;Keywords: glycoprotein; transmembrane protein
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-1173/Product: E2 glycoprotein #status predicted <MAT>
F;1116-1138/Domain: transmembrane #status predicted <TMN>
F;23,62,98,147,171,176,220,243,326,333,440,464,518,538,542,568,581,587,663,671,930,1015
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A; Molecule type: mRNA
A; Residues: 1-1173 < RAA>
A; Cross references: EMBL:X16816; NID:958926;
A; Cross references: strain 229E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Raabe, T.; Siddell, S.
Nucleic Acids Res. 17, 6387, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Title: Nucleotide
A; Reference number:
A; Accession: A34766
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A;Recession: T12505
A;Stature: T12505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1159-1173 <RA2>
                                                                                            hypothetical protein C50F7.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T29295
R;Johnson, D.; Stellyes, L.
Submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid C50F7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Ansorge, W.; Wirkner, U
submitted to the Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein DKFZp434C192.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999
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A;Experimental source: adult testis;
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A; Residues: 1-299 < ANS>
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A; Molecule type: DNA
A; Residues: 1-111 < JOH>
                                                       A;Description: The sequence
A;Reference number: Z20601
A;Accession: T29295
                                  A; Status: preliminary; translated from GB/EMBL/DDBJ
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nce number: A34766; 1
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Database, June 1999
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A;Cross-references: EMBL:U41557; PIDN:AAA83303.1; CESP:C50F7.8 C;Genetics: A;Gene: CESP:C50F7.8
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Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating A;Reference number: A75000; MUID:99069613; PMID:9851916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein F18G5.2 [imported] - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 10-May-2001 #sequence_revision 10-May-2001 C;Accession: E89605
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                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Bos primigenius taurus (cattle)
C;Date: 14-Jul-1994 #sequence_revision 18-oct-1996 #text_change 03-Jun-2002
C;Accession: JT0751; JT0079; JS0390; S03558; PS0003; A29604; S52100
R;Takata, Y; Sagara, Y; Kono, A.; Sekimizu, K.; Horiuchi, T.
BiOl. Pharm. Bull. 16, 1200-1206, 1993
A;Title: Gene structure of bovine adrenodoxin reductase...
A;Reference number: JT0751; MUID:94177140; PMID:8130767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-467 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_A;Note: published_errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;
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                                                            A;Title: Cloning and sequence analysis of adrenodoxin reductase A;Reference number: JT0079; MUID:88198050; PMID:3448086
A;Reference number: JT0079; MUID:88198050; PMID:3448086
A;Accession: JT0079
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-204,211-498 <SAG>
A;Cross-references: GB:D00211; NID:g217433; PIDN:BAA00150.1; PIDA;Note: the deduced sequence is partially confirmed by amino aci
                                                                                                                                                                                                                  A;Note: the authors translated the codon GTC for residue 205 R;Sagara, Y.; Takata, Y.; Miyata, T.; Hara, T.; Horiuchi, T. J. Biochem. 102, 1333-1336, 1987
                                                                                                                                                                                                                                                                                     A;Residues: 1-498 <TAK>
A;Cross-references: GB:D83475; NID:g1199916; PIDN:BAA11921.1; PID:g4521308
A;Experimental source: adrenal cortex
submitted to DDBJ, September 1989 A; Reference number: JS0390
                                                                                                                                                                                                                                                                                                                                    A; Molecule type:
A; Residues: 1-49
                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: JT0751
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83.3%;
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Pred. No.
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Pred. No. 4.2;
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22;
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revision,

insertion of

residues 205-210

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A; Molecule type: protein
A; Residues: 33-41,'S',43-62;260-283,'TM';496-498 <HAM>
A; Residues: 33-41,'S',43-62;260-283,'TM';496-498 <HAM>
A; Note: a cyanogen bromide peptide binds to adrenoferredoxin
R; Nonaka, Y.; Murakami, H.; Yabusaki, Y.; Kuramitsu, S.; Kagamiyama, H.; Yamano, T.; Oka
Biochem. Biophys. Res. Commun. 145, 1239-1247, 1987
A;Title: Molecular cloning and sequence analysis of full-length cDNA for mRNA of adrenod
A; Reference number: A29604; MUID:87270696; PMID:3038094
A; Molecular cloning and sequence analysis of full-length cDNA for mRNA of adrenod
A; Reference number: A29604; MUID:87270696; PMID:3038094
A; Molecular cloning and sequence analysis of full-length cDNA for mRNA of adrenod
                                                                                       hypothetical protein SCE36.09 - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 C;Accession: T36208 R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajanc submitted to the EMBL Data Library, May 1999
                                                                                                                                                                                                                                                                                                    RESULT 7
T36208
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A;Residues: 1-76,'K',78-80,'VWLALTTPRSRMLL',95-123,'RVYRLT',129-204,211-273,'R',275-322,
A;Cross-references: GB:M17029; NID:g162628; PIDN:AAA30362.1; PID:g162629
A;Experimental source: adrenal cortex
R;Warburton, R.J.; Seybert, D.W.
Biochim. Biophys. Acta 1246, 39-46, 1995
A;Title: Structural and functional characterization of bovine adrenodoxin reductase by l
A;Reference number: S52100; MUID:95110846; PMID:7811729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Keywords: alternative splicing; flavoprotein; mitochondrion; monomer; NADP; oxidoreduo
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A;Residues: 'X',34-41,'X',43-48,'X',50-51;304-306,'X',308-309,'X',311-326 <WAR>
C;Comment: Ferredoxin NADP+ reductase is localized in the matrix of adrenal cortex mitocerredoxin NADP+ reductase, adrenodoxin and two forms of cytochrome P-450.
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A;Title: Adrenoferredoxin-binding peptide of NADPH-adrenoferredoxin reductase.
A;Reference number: PS0003; MUID:88184054; PMID:3355838
A;Accession: PS0003
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A;Residues: 155-204,211-498 <HAN>
A;Cross-references: EMBL:X13736; NID:g65;
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   A;Status:
                                      A;Reference number: Z21601
A;Accession: T36208
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   preliminary;
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5; Conserv
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translated
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83.3%;
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07-213, 1988
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   from GB/EMBL/DDBJ
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MAMMA

Matches Query Match Best Local

FOCGT

Similarity 5; Conserv

54.7%;

Score 47; Pred. No.

DB 22,

0;

Gaps

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0;

A; Molecule type: protein A; Residues: 1-32 < PAR1>

F;1-248/Product: NADH oxidase (H2O2-forming) #status experimental

C; Keywords: NAD; A; Gene: nox

oxidoreductase

Genetics

A;Cross-references: EMBL:X60110 A;Accession: S24556

A; Molecule type: DNA A; Residues: 1-248 < PAR>

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R;Park, H.J.; Kreutzer, R.; Reiser, C.O.A.; Sprinzl, M. Eur. J. Biochem. 205, 875-879, 1992
A;Title: Molecular cloning and nucleotide sequence of the A;Reference number: S23449; MUID:92249331; PMID:1577004
A;Accession: S23449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Date: 09-Nov-2001 *sequence_revision C;Accession: AH0755 R;Parkhill, J.; Dougan, G.; James, K.D. th, T.; Connerton, P.; Cronin, A.; Davi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:AL049763; PIDN:CAB42078.1; A;Experimental source: strain A3(2) C;Genetics: A;Gene: SCOEDB:SCE36.09
                                                                                                                                                                            NADH oxidase (H2O2-forming) (EC 1.6.-.) - Thermus aquaticus C;Species: Thermus aquaticus C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change C;Accession: S23449; S24556
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Nature 413, 848-852, 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-265 < PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: AB0502; A; Accession: AH0755
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Best Local S
Matches 6
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8; Conserv
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31.6%;
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Pred. No. 17;
3; Mismatches
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Pred. No. 6.
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Davis, P.; Davies, R.
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17;
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; White, N.
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Ho Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complet A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: G70715
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A;Residues: 1-253 <COL>
A;Cross-references: GB:Z79700; GB:AL123456; NID:g3261628; PIDN:CAB02005.1; PID:g1524217
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: Rv0945
A;Gene: Rv0945
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
F;8-190/Domain: short-chain alcohol dehydrogenase homology
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: G70715
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C;Superf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: B83161
                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE004805; GB:AE004091; A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Complete genome sec
A;Reference number: A82950;
A;Accession: B83161
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probable moeY protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 2
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                                                                                        RESULT 12
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Best Local
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5; Conserv
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Conservative
                                                                                                                                                                                                                                            Conservative
    #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence of Pseudomonas aeruginosa PAO1, an 50; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                   54.7%;
70.0%;
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Pred. No.
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Pred. No. 24;
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C;Accession: B70741
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Authors: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Recession: B70741
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Residues: 1-715 cOLl-A;Residues: 1-715 cOLL-A;Residues: 1-715 cOLL-A;Residues: 1-715 cOLL-A;Residues: Strain H37Rv
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-1411 <BEV>
A; Cross-references: EMBL: AL163814
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A; Introns: 281/2;
A; Note: T22P22.90
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A; Accession: T48529
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                                                                                                                                                                     R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, submitted to the Protein Sequence Database, July 2000
                                                                                                                                                                                                                     C; Accession: T51071
                                                                                                                                                                                                                                            related to trfA protein [imported] - Neurospora crassa N;Alternate names: protein B2A19.50 C;Species: Neurospora crassa C;Species: Neurospora crassa C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
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A; Experimental source:
                         A;Cross-references: EMBL:AL390092; GSPDB:GN00116; NCSP:B2A19.50
                                                A; Molecule type: DNA
A; Residues: 1-728 <SCH>
                                                                                                                     A; Reference number: Z25286
A; Accession: T51071
                                                                                              A; Status: preliminary
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Best Local S
Matches 6
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Local Similarity 63.6%;
nes 7; Conservation
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     BAC clone B2A19; strain OR74A
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anthranilate synthase (EC 4.1.3.27) component I [validated] - Pseudomonas syringae pv. st. Alternate names: anthranilate synthase alpha chain C:Species: Pseudomonas syringae pv. savastanoi C:Date: 27-Nov-1991 **sequence_revision 27-Nov-1991 **text_change 17-Mar-2000 C:Accession: A39128 R:da Costa, E.; Silva, O.; Kosuge, T. J. Bacteriol. 173, 463-471, 1991 A:Reference number: A39128; MUID:91100331; PMID:1987141 A:Reference number: A39128; MUID:91100331; PMID:1987141 A:Costasion: A39128
                                                                                                                                                                                                                                                       A;Description: EC 4.1.3.27 (validated, MUID:91100331]
A;Note: expression of trpE seems to be independent of the concentration of tryptophan in C;Superfamily: anthranilate synthase component I C;Keywords: carbon-carbon lyase; oxo-acid-lyase; tryptophan biosynthesis
                                                                                                                                                                                                                                                                                                                                                  A;Gene: trpE
C;Complex: heterotetramer; two component I chains, two component II chains
C;Function: <ANT>
A;Description: EC 4.1.3.27 [validated, MUID:90130325]
A;Pathway: tryptophan biosynthesis
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A;Note: first step
C;Function: <COM1>
Search completed: January 15, 2003, 18:04:27 Job time: 17 secs
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Q09677 schizosacch
Q63085 rattus norv
P21217 homo sapien
Q19058 pan troglod
Q10773 mycobacteri
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01-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
E2 glycoprotein precursor (Spike glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Raabe T., Schelle-Prinz B., Siddell S.G.;

"Nucleotide sequence of the gene encoding the spike glycoprotein human coronavirus HCV 229E.";

J. Gen. Virol. 71:1065-1073(1990).

-i- FUNCTION: THE PEPLOMER PROTEIN MEDIATES THE BINDING OF VIRION TO THE HOST CELL RECEPTOR AND IS INVOLVED IN MEMBRANE FUSION AND IN SYNCYTION FORMATION.

-i- SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human coronavirus (strain 229E).
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
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CARBOHYD
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Pred. No. 0.0051;
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15-JUL-1998 (Rel. (
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
NADPH:adrenodoxin oxidoreductase, mitochondrial precursor
(EC 1.18.1.2) (Adrenodoxin reductase) (AR) (Ferredoxin-NADP(+)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pec
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TISSUE-Adrenal cortex;
MEDLINE-89170752; PubMed-2924777;
Hanukoglu I., Gutfinger T.;
"cDNA sequence of adrenodoxin reductase.
binding sites in oxidoreductases.";
                                                                    Yamano T., Okamoto M.;
"Molecular cloning and sequence analysis of full-length cDNA
of adrenodoxin oxidoreductase from bovine adrenal cortex.";
piccham Biophys. Res. Commun. 145:1239-1247(1987).
                                                                                                                                                                Sagara Y., Takata Y., Miyata T. "Cloning and sequence analysis bovine adrenal cortex.";
                                                                                                                                                                                                                           "Gene structure of bovine adrenodoxin reductase Biol. Pharm. Bull. 16:1200-1206(1993).
                                                                                                               MEDLINE-87270696; PubMed=3038094;
MEDLINE-87270696; PubMed=3038094;
Nonaka Y., Murakami H., Yabusaki Y.,
                                                                                                                                             J. Biochem. 102:1333-1336(1987).
                                                                                                                                                                                             SEQUENCE FROM N.A., AND PARTIAL SEQUENCE MEDLINE-88198050; PubMed=3448086;
                                                                                                                                                                                                                                                                                                 Bovidae;
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177140; PubMed=8130767;
Sagara Y., Kono A., Sekimizu K., I
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"Adrenodoxin reductase-adrenodoxin complex structure suggests e
transfer path in steroid biosynthesis.";
J. Biol. Chem. 276:2786-2789(2001).

-I- FUNCTION: SERVES AS THE FIRST ELECTRON TRANSFER PROTEIN IN
MITOCHONDRIAL P450 SYSTEMS. INCLUDING-CHOLESTEROL SIDE CHAI
CLEAVAGE IN ALL STROUIDOZENIC TISSUES, STEROID 11-BETA
HYDROXYLATION IN THE KIDNEY, AND STEROL C-27 HYDROXYLATION
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"Isolation of a cDNA for adrenodoxin reduc
reductase). Implications for mitochondrial
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MEDLINE=20455764; PubMed=109
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"Crystal structures of adrenodoxin
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3L; D83475; BAA11921.1;
JB; D83472; BAA11921.1;
JL; D83473; BAA11921.1;
JL; D83474; BAA11921.1;
JL; D83474; BAA11921.1;
JL; D00211; BAA00352.1;
L; D00211; BAA00350.1;
L; X13736; CAA32002.1;
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CATALYTIC ACTIVITY:
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ALTERNATIVE PRODUCTS: 2 ISOFORMS; A SHORT FORM (SHOWN HERE) AND A LONG FORM; ARE PRODUCED BY ALTERNATIVE SPLICING. THE LONG FORM REPRESENTS 10-20% OF ALL ADRENODOXIN REDUCTASE MRNA. AND SEEMS TO
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative oxidoreductase RV0945 (EC 1.-.-).
RV0945 OR MT0971 OR MTCY10D7.29C.
                                                                                                                    laboratory strains.";
Submitted (APR-2001) to
-!- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D
                                                                                                                                                                                                                                                                                                                                                             "Deciphering the biology of Mycobacterium tuberculosis from complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
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s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Ew European Bioinformatics Institute. There are no restr by non-profit institutions as long as its content
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RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Geborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Rutter S., Seeger K., Whitehead S., Barrell B.G.;
TDeciphering the biology of Mycobacterium tuberculosis from the
Complete genome sequence ";
L. Nature 393:537-544(1998).
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                                                                                                                                                                                                                                                                                                         SEQUENCE FAVOR ..... SHAIN-GEO 1551 / Oshkosh; STRAIN-CDC 1551 / Oshkosh; STRAIN-CDC 1551 / Oshkosh; Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White Creates and J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey Reterson J., DeBoy R., Dodson R., Gwinn M.L., Ermolaeva M.D., Salzbe Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzbe Kolonay J.F., Nelson W.C., Umayam L.A., Khouri H., Gill J., Mikk
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01-OCT-1996 (Rel. 34, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Hypothetical protein Rv1355c.
Rv1355c OR MT1398 OR MTCY02B10.19C.
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01-OCT-1996
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Hypothetical protein; Oxidoreductase; Complete ACT_SITE 159 159 BY SIMILARITY.
                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration -
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                                                                                                                                                                                                                              Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                        {\tt W}{\tt M}{\tt hole} genome comparison of {\tt Mycobacterium} tuberculosis laboratory strains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis
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TUBERCULLIST; Rv1355c; -.
TUBERCULLIST; Rv1355c; -.
InterPro; IPR000594; ThiF_domain.
Pfam; PF00899; ThiF; 1.
Pfam; PF00899; ThiF; 1.
Hypothetical protein; Complete proteome.
Hypothetical protein; Complete proteome.
715 AA; 78181 MW; 455495248A56041C CRC64;
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or send a
                                                                                                                                                                                                            EMBL; M55911; AAA26016.1; -.
pir; A39128; A39128.
HSSP; Q06128; 1QDL.
InterPro; IPR005256; Anth_synth1.
InterPro; IPR000350; Chorismate_bind.
Pfam; PF00425; chorismate_bind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pyruvate + L-glutamate.
-!- PATHWAY: Tryptophan biosynthesis; first
-!- SUBUNIT: TETRAMER OF TWO COMPONENTS I AN
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         da Costa e Silva O., Kosuge T.,
"Molecular characterization and
anthranilate synthase gene of Ps
savastanoi.";
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01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last seq
15-JUN-2002 (Rel. 11, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed.
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-!- CATALYTIC ACTIVITY: Chorismate + L-glutamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=91100331; PubMed=1987141;
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TIGR; MT1398;
                                                                                              Tryptophan
SEQUENCE
                                                                                                                                                                    PRINTS; PR00095; ANTSNTHASEI.
ProDom; PD000779; Chorismate_bind;
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                                                                                                                                         TIGRFAMs; TIGR00564; trpE_most; 1.
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                                                                                                                                                                                                                                                                                                                                                                                   s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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Similarity 7; Conserv
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Pred. No.
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RA Gentles S., Goble A., Hamlin N., Harris D., Hadalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Ra Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Raylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Gailbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Gailbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RI Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RI Nature 415:871-880(2002).
CC '(MDAB)
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Q09677;
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content endified and this statement is not removed. Usage by an entities requires a license agreement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
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Pfam; PF02525; NADHdh_2; 1.
                                                                                                                                                                                                                                                                                                                                              EMBL; Z49811; CAA89955.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
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(Rel. 41,
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etales; Schizosaccharomycetaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Thes 5; Conserve
    FUT3_HUMAN S:
P21217; Q99448; (
P1-21217; Q994
                                                                                                                                                                                                                                             HUMAN
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J. Biol. Chem. 268:18573-18579(1993).
-i- FUNCTION: MAY PLAY A ROLE IN FAT METABOLISM.
-i- CATALYTIC ACTIVITY: Nucleoside 3',5'-cyclic phosphate.
-i- CATALYTIC ACTIVITY: Nucleoside 3',5'-cyclic phosphate.
-i- ENZYME REGULATION: INHIBITED BY CGMP.
-i- SUBCELLULAR LOCATION: Membrane-bound (Potential).
-i- TISSUE SPECIFICITY: ABUNDANT IN ADIPOSE TISSUES.
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15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
cGMP-inhibited 3',5'-cyclic phosphodiesterase B (EC 3.1.4.17) (Cyclic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sentitles.com/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/discom/dis
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Ъ Š ALD DEPTH TO DESCRIPTION OF THE PROPERTY OF TH

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Kukowska-Latallo J.F., Larsen R.D., Nair R.P., I "A cloned human cDNA determines expression of a embryonic antigen and the Lewis blood group alpha(1,3/1,4) fucosyltransferase.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Galactoside 3(4)-L-fucosyltransferase (EC 2.4.1.65) (Blood group Lewis alpha-4-fucosyltransferase) (Lewis FT) (Fucosyltransferase 3) (FUCT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95378269: PubMed=7650030;
Cameron H.S., Szczepaniak D., Weston W.;
"Expression of human chromosome 19p alpha(1,3)-fucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=91032981;
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                                                                                                                                                                                                                                                                                                            "Alpha (1,3/1,4)fucosyltransferase (FucT-III) gene a single amino acid substitution in Lewis histo-bio individuals.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rahim I., Schmidt L.R., Wahl D., Drayson E., Maslan Stranahan P.L., Pettijohn D.E.; "Isolation and expression of human alpha (1,3/1,4) fucosyltransferase.";
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                      *Genotypic heterogeneity among
                                                                                                                   VARIANTS LE(-) ARG-20 AND LYS-356.
MEDLINB=94342259; PubMed-8063716;
MO11cone R. Reguigne I., Kelly R.J., Fletcher A., Watt J.,
Chatfield S., Aziz A., Cameron H.S., Weston B.W., Lowe J.B.,
"Molecular basis for Lewis alpha(1,3/1,4)-fucosyltransferase
deficiency (FUT3) found in Lewis negative Indonesian pedigree
J. Biol. Chem. 269:20987-20994(1994).
                                                                                                                                                                                                                Blood 82:2915-2919(1993).
                                                                                                                                                                                                                                                                VARIANTS LE(-) ARG-20 MEDLINE-94033579; Pub
                                                                                                                                                                                                                                                                                                                                                            Nishihara S., Yazawa S.,
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MEDLINE=94059082; PubMed=8240337
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                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94059067;
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                                   system.",
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                                                                                                                                                                                                                                                      Koda Y., Kimura H.,
 VARIANTS
                                                           Ando
                                                                                MEDLINE=95050753;
                                             "Molecular genetic
                      Biol.
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LE(-)
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                                                         Narimatsu H.,
T., Narimatsu
                                                                                             LYS-356
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 ARG-20;
                         269:29271-29278(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cell carcinoma;
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                                                                                                                                                                                                                                                                G-20 AND SER-170.
PubMed=8219240;
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                                                                                  PubMed=7961897;
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Primates;
                                              analysis
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  ARG-68; MET-105
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                                                                                                                                                                                                                                                                                                                                                              Iwasaki H.,
                                              I.;
of the human
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                                                                                                                                                                                                                              -negative
                                                                                                                                                                                                                                                                                                                                                                                                            Lewis negative individuals."; 196:515-520(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                      G.;
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e individuals.";
  AND LYS-356
                                                                        Yazawa
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'FUT3' gene enables molecular group system.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Elmgren A., Boerjeson C., Svensson L., Rydberg L., Larson G.; "DNA sequencing and screening for point mutations in the human Lewis 'FUT3' gene enables molecular genotyping of the human Lewis blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Elmgren A., Mollicone R.,
Harrington J., Larson G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96243526; PubMed=8801770;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANTS LE(-) ARG-68 AND MET-105.
MEDLINE=97413801; PubMed=9268337;
                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Dutstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                        EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FORM IN TRANS CISTERNAE OF GOLGI.

FORM IN TRANS CISTERNAE OF GOLGI.

TISSUE SPECIFICITY: HIGHLY EXPRESSED IN STOMACH, COLON, SMALIVARISTINE, LUNG AND KIDNEY AND TO A LESSER EXTENT IN SALIVARIANCE, LUNG AND LIVER.

GLAND, BLADDER, UTERUS AND LIVER.

MISCELLANEOUS: ALSO ACTS ON THE CORRESPONDING 1,4-GALACTOSYL DERIVATIVE, FORMING 1,3-L-FUCOSYL LINKS.

SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PATHWAY: Glycosylation: TYPE II MEMBRANE PROTEIN.
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
TO THE TRANSPORTER OF GOLGI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INVOLVED IN THE EXPRESSION OF VIM-2, LEWIS A, LEWIS B, SIALYL LEWIS X AND LEWIS X/SSEA-1 ANTIGENS. MAY BE INVOLVED IN BLOOD GROUP LEWIS DETERMINATION; LEWIS-POSITIVE (LE(+)) INDIVIDUALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: GDP-L-fucose + 1,3-beta-D-galactosyl-N-acetyl-D-glucosaminyl-R = GDP + 1,3-beta-D-galactosyl-(alpha-1,4-fucosyl)-N-acetyl-D-glucosaminyl-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAVE AN ACTIVE ENZYME WHILE LEWIS-NEGATIVE (LE(-)) INDIVIDUALS HAVE AN INACTIVE ENZYME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genet. 102:675-680(1998).
FUNCTION: MAY CATALYZE ALPHA-1,3 AND ALPHA-1,4 GLYCOSIDIC
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DOMAIN CARBOHYD CARBOHYD EMBL; D89324; BAA13941. EMBL; D89325; BAA13942. EMBL; AF131913; AAD3351 PIR; A36669; A36669; EMBL; MIM; Genew; VARIANT Signal-anchor; Transferase; Pfam; PF00852; VARIANT TRANSMEM DOMAIN InterPro; x53578; CAA37641.1; -.
; U27328; AAC50187.1; -.
; U27326; AAC50185.1; -.
; U27327; AAC50186.1; -.
; D89324; BAA13941.1; -.
; D89325; BAA13942.1; -. HGNC:4014; FUT3. IPR001503; GT_10 16 35 154 185 20 Glyco_transf_10; 1.
 Glycosyltransferase; Glycoprotein; Transmembrane; Golgi AAD33514.1; 15 stack; 15 stack; 15 34 361 361 154 185 20 X; Polymorphism; Blood group antigen.
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
LUMENAL, CATALYTIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (PROBABLE).
N-LINKED (GLCNAC. . .) (PROBABLE).
L -> R (IN LE(-)).
/FTId=VAR.003456.
W -> R (IN LE(-)).

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Matches
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30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 4), Last annotation update)
Galactoside 3(4)-L-fucosyltransferase (EC 2.4.1.65) (Blood alpha-4-fucosyltransferase) (Lewis FT) (Fucosyltransferase III) (Alpha-3/4-fucosyltransferase).
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Mammalia; Eutheria;
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                                                                                        CATALYTIC ACTIVITY: GDP-L-fucose + 1,3-beta-D-galactosyl-N-acetyl-D-glucosaminyl-R = GDP + 1,3-beta-D-galactosyl-(alpha-L-fucosyl)-N-acetyl-D-glucosaminyl-R.

1.4-L-fucosyl)-N-acetyl-D-glucosaminyl-R.

PATHWAY: Glycosylation.

PATHWAY: Glycosylation: TYPE II MEMBRANE PROTEIN. MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI (BY SIMILARITY).

POLYMORPHISM: THERE ARE TWO ALLELES (A AND B). ALLELE A HAS ARC 162 AND WAL-304. ALLELE B HAS GLY-162 AND MEMBRANE-BOUND FORM AND ALLELE B HAS GLY-162 AND MEMBRANE-BOUND FORM AND MEMBRANE-BOUND FORM IN TRANS CISTERNAE OF GOLGI (BY SIMILARITY).
SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in ....
                                                     MISCELLANEOUS: ALSO ACTS ON THE CORRESPONDING 1 DERIVATIVE, FORMING 1,3-L-FUCOSYL LINKS.
SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE
                                                                                                                                                                                          (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                               (Chimpanzee).
zoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 356
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85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G -> S (IN LE(-); CC /FTId=VAR_003428. G -> R (IN LE(-)). /FTId=VAR_007963. V -> M (IN LE(-)). /FTId=VAR_007964. D -> A (IN LE(-)). /FTId=VAR_003429.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
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Q -> K (IN LE(+)).

/FTId=VAR_007960.

T -> M (IN LE(-)).
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Pred.
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IN ACTIVITY).
                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /FTId=VAR_003430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /FTId=VAR_007962.
G -> S (IN LE(-); COMPLETELY INACTIVE).
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D -> N (IN LE(-))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T -> M (IN LE(-)).
/FTId=VAR_003427.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BF4398044F19C284
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                                                       FAMILY
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3) (FUCT-
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RESULT 11
MML6_MYCTU
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Best Local
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01-OCT-1996
16-OCT-2001
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CARBOHYD
VARIANT
VARIANT
                                                    "Whole genome comparison of Mycobacterium tube laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ-1- SUBCELLULAR LOCATION: Integral membrane pr-1- SIMILARITY: BELONGS TO THE MMPL FAMILY.
                                                                                                                                     STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                   Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis complete genome sequence."; Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                             Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MML6_MYCTU Q10773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MMPL6 OR RV1557 OR MT1608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00852; Glyco_transf_10; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane.
                                                                                                                            Bishai W.;
                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98295987;
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Actinomycetales; Corynebacterineae; NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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PQWPWRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 34, Createa)
(Rel. 34, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            372 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35
165
196
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1 CYTOPLASMIC
SIGNAL-ANCHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                           PubMed=9634230;
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85.7%;
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LUMENAL, CATALYTIC (P. N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
R-> G (IN ALLELE B).
V -> M (IN ALLELE B).
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL-ANCHOR (TYPE-II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          649CBF8BCA7BD74C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                    membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                teria (class); Actinobacteridae;
Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28;
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                                                                                                              tuberculosis clinical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Usage
                                                                 databases.
rotein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
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                RA COLLINS M., CONDOOR M., HARTIS D., Heltwell T., Fraser A.,
RA COLLINS M., CONDOOR M., HARTIS D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
A James K., Jones M., Leather S., McDonald S., McLean J.,
RA James K., Jones M., Leather S., McDonald S., McLean J.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA McDoney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA McDer G., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Raylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Raylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Welljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Welljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
Galilardin C., Tallada V.A., Garzon A., Thode G.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., Gerzon A., Thode G.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
The genome sequence of Schizosaccharomyces pombe.";
The genome sequence of Schizosaccharomyces pombe.";
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Best Local
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or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1998 (Rel. 36, Created)
15-JUN-2008 (Rel. 36, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Hypothetical protein C23C1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
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entities requires a license
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schizosaccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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uList; Rv155',
pro; IPR004869; MMPL.
pF03176; MMPL; 1.
potein; Transmembrane; Com
potein; Transmembrane; Transmembrane; Com
potein; Transmembrane; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Z74020; CAA98334.1; -. AE007027; AAK45875.1;
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6; Conserv
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RESULT 13
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                                                                                                                                                                                                                            RX MEDLINE=88295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris I RA Cole S.T., Brosch R., Parkhill J., Barry C.E. III, Tekaia F., RA Gordon S.V., Elglmeler K., Gas S., Barry C.E. III, Tekaia F., RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R., RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., RA Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J., RA Oliver S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; L. Nature 393:537-544(1998).
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Best Local S
Matches
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053735;
30-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as IVWY .... By non-profit institutions as IVWY .... Usage by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed.
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30-MAY-2000 (Rel.
16-OCT-2001 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Putative membrane protein mmpL4.
MMPL4 OR RV0450C OR MT0466 OR MTV037.14C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Actinomycetales;
                                           laboratory strains.";
Submitted (APR-2001) to the subcellular Location:
-!- SUBCELLULAR LOCATION:
                                                                                                                                 Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg thelefer A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN=CDC 1551 /
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Actinobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 WSWSPSTWPWRQ 194
This SWISS-PROT entry is copyright. between the Swiss Institute of Bio:
                                                                                                                       Bishai W.;
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Corynebacterineae; Mycobacteriaceae; Mycobacterium
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39, Last sequence up
40, Last annotation
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Pred. No. 40;
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Bioinformatics and the EMBL outstation ~
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GCole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G., "Decipharing the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
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Pfam; PF0
SEQUENCE FROM N.A.

STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula Bishai W.;
                                                                                                                                                                                                                                                                                                                01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence up
16-OCT-2011 (Rel. 40, Last annotation
Putative membrane protein mmpL2.
MMPL2 OR RV0507 OR MT0528 OR MTCY20G9.
                                                                                                                                                                                                                                                                                                                                                                                                 MYCTU
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Q11171;
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AE006949; AAK44689.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             d and this statement is not removed. Usage by and for commercial s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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RESULT 15
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                                                                                                                            Roose J., Korver W., Ovi
Lamers W., Clevers H.;
"High expression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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TISSUE=Embryo;
MEDLINE=98201614; PubMed=9524265;
                                                                                                                                                                                 MEDLINE-98083175; PubMed-9421502; Roose J., Korver W., Oving E., Wilson A.,
                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                   SOX-13 protein
SOX13 OR SOX-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SX13_MOUSE
Q04891;
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                                                                                              Nucleic
                                                                                                                  embryonic
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                                                                                                                                                                                                                                                               SEQUENCE
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Rodentia;
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Search completed: January 15, 2003, 18:03:28 Job time: 13 secs
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Best Local (
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EMBL; 218652; CAA79487.1;
PIR; S30241; S30241
HSSP; Q05066; 1HRY.
MGD; MGI:98361; Sox13.
InterPro; 1PR0050910; HMG_12_box.
Pfam; PF00505; HMG_box; 1.
SMART; SM00398; HMG; 1.
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"Cloning and characterization of mouse mSox13 cDNA.";
Gene 208:201-206(1998).
[3]
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MEDLINE-93181275; PubMed-8441686;
MIDITUME-93181275; PubMed-8441686;
MIDITUME-93181275; PubMed-8441686;
MIDITUME-93181275; PubMed-8441686;
MIDITUME MEMBERS OF THE SEQUENCE 5'-AACAAT-3'.
-!- FUNCTION: BINDS TO THE SEQUENCE 5'-AACAAT-3'.
-!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
-!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
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ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; MAY BE PRODUCED BY ALTERNATIVE SPLICING.

PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: IN THE EMBRYO, HIGH LEVELS OF EXPRESSION ARE FOUND IN THE ARTERIAL WALLS AT 13.5 DAYS POST COLTUM (DPC). LOW FOUND IN THE INNER EAR AT 13.5 DPC AND IN SOME CELLS IN THE THYMUS AT 16.5 DPC. EXPRESSED IN THE TRACHEAL EPITHELIUM BELOW THE THYMUS AT 16.5 DPC. EXPRESSED IN THE TRACHEAL EPITHELIUM BELOW THE VOCAL CORD AND IN THE HAIR FOLLICLES AT 18 DPC.

SIMILARITY: CONTAINS 1 HMG BOX.
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610
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984 AA;
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159 195 GLN-RICH.
397 465 HMG BOX.
495 519 PGCSPKLHHPVSRPSLVARGGLA
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985 P
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42 AT
195 Q
195 Q
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42.9%;
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MISSING (IN ISOFORM 2).
P -> L (IN REF. 2).
AT -> TN (IN REF. 2).
Q -> QQ (IN REF. 2).
Q -> QQ (IN REF. 2).
                                                                                                                                                                                                                                                                        Score 44; DB 1; Length 984; Pred. No. 70;
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HMG BOX.
PGCSPKLHHPVSRPSLVARGGLWLL -> QGARQSYTIP
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Result
No.
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Listing first 45 summaries
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SP_Archea:*

Sp_bacteris*

Sp_bacteris*

Sp_fungi:*

Sp_human:'

Sp_invert

Sp_mamma

Sp_mac:

Sp_mac:

Sp_pha

10:
Sp_pha

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Sp_r

12:
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13:
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15:
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17:
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length: 2000000000
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86
1 ILRWPWWPWRRK 1:
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                                                                                                                                                                                                                                                                sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
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sp_bacteria:*
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sp_mammal:*
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Q9CZA1
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(without alignments)
85.261 Million cell updates/sec
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                             O9duc4 tt virus. o
O99dna human coron
O94712 porcine epi
O84712 porcine epi
O84794 porcine epi
O8498 porcine epi
O8498 porcine epi
O8498 porcine epi
O8498 porcine epi
O94745 trichoderma
O84040 porcine
O9411 thermoactin
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Q9czal mus musculu
Q9aun3 oryza sativ
Q9duc9 tt virus. o
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45	45	45	45	45	45	45	45	45	45.5	46	46	46	47	47	47	47	47	48	48	48	48.5	49	49	49	49	49	49	49
52.3		2	2.	2	.2	52.3	2	2	2	ω	w	ω.	4.	54.7	54.7	54.7	4.	5	55.8	5	56.4	57.0	7.	57.0	57.0	7.	7.	57.0
443	423	412	342	273	187	159	150	134	175	521	257	154	1411	734	276	165	92	540	265	265	114	750	748	606	467	226	226	49
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Q9S751	024742	Q916F7	Q96BE4	Q9PCR3	Q8YHI9	Q9KZT3	Q8S697	Q96UD2	Q91RD8	Q94EF3	Q8TWW9	Q9R6J3	Q9LYG0	Q8V7I1	Q9нxс9	Q9SNN3	Q8V7E2	007504	Q8Z5Q0	Q82NS5	Q9x8C2	Q91D04	Q9DT81	Q988W4	Q19573	Q9BSG8	Q96LL9	Q9DT80
Q9s751 oryza sativ	024742 bacteroides	Q916f7 pseudomonas	Q96be4 homo sapien	Q9pcr3 xylella fas			7	Q96ud2 neurospora			Q8tww9 methanopyru	Q9r6j3 agrobacteri	arabidopsi			oryza sati	Q8v7e2 tt virus. o								Q19573 caenorhabdi	homo	nomo sapier	Q9dt80 tt virus. o

ALIGNMENTS

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Matches 7
                                                                                        phylogenetic relatedness.";
Virology 277:368-378(2000).
EMBL; AB041959; BAB19313.1;
Interpro; IPR001563; Serine_carbpept.
Interpro; IPR004219; TTvirus_Unk.
Pfam; PF02956; TT_ORF1; 1
PROSITE; PS00131; CARBOXYPEPT_SER_SER; UNKNOWN_1.
SEQUENCE 723 AA; 85393 MW; 232D003098766344 CRC64;
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01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                              ORF1.
TT virus.
Viruses; ssDNA viruses;
                                                                                                                                                                                     MEDLINE=20534983; PubMed=11080484;
Okamoto H., Nishizawa T., Tawara A., Peng Y., Takahashi M.,
Kishimoto J., Tanaka T., Miyakawa Y., Mayumi M.;
"Species-specific TT viruses in humans and nonhuman primates and their
                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9DUC4
                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=MF-TTV9;
                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=68887;
                                                                                                                                                                                                                                                                        Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                     Okamoto H.;
                                                                                                                                                                                                                                                                                                 STRAIN-MF-TTV9;
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           5 PWWPWRR 11
2 PWWPWRR 8
                                              Similarity
7; Conserv
                                              Conservative
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                                            66.3%; Score 57; DB
100.0%; Pred. No. 8.1
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                unclassified ssDNA viruses
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Last annotation update)
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                                                              Query Match
Best Local Similarity Matches 5; Conserv
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01-OCT-2000
01-OCT-2000
01-JUN-2002
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                                                                                                                                "Viral and cellular changes in a human cell line persistently infected with human coronavirus HCOV-229E.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF344186; AAK32188.1; ...
InterPro; IPR002551; Corona_S1.
InterPro; IPR002551; Corona_S2.
Pfam; PF01600; Corona_S2; 1.
Pfam; PF01601; Corona_S2; 1.
SEQUENCE 1173 AA; 128669 MW; ABC6E0A75E8BD8A4 CRC64;
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01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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Interpro; IPR004219; TTVirus_Unk.
Pfam; PF02956; TT_ORF1; 1.
SEQUENCE 746 AA; 88561 MW; E0
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Ukita M., Okamoto H., Nishizawa T., Tawara A., Takahashi M
Iizuka H., Miyakawa Y., Mayumi M.;
"The entire nucleotide sequences of two distinct TT virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-TJN02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; ssRNA positive-strand viruses, Coronaviridae; Coronavirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=11137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spike glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bonavia A., Holmes K.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=229E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human coronavirus (strain 229E)
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   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88561 MW; E0B22953AE764E3E CRC64;
                                    61.6%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61.6%;
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15,
21,
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Pred.
                                    Pred. No. 42;
                                                                      Score 53; DB 12;
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Best Local Similarity
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Q990M3;
01-JUN-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
                                                                                                                                                                                                                                                                                                      Q990M2 PRELIMINARY;
Q990M2;
01-JUN-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
                                                                                "Viral and cellular changes in a human cell line persistently infected with human coronavirus HCOV-229E."; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF344188; AAK32190.1; ...
InterPro; IPR002551; Corona_S1.
InterPro; IPR002551; Corona_S1.
Pfam; PF01600; Corona_S1; 1.

Pfam; PF01601; Corona_S2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human coronavirus (strain 229E).
Viruses; ssRNA positive-strand viruses,
Coronaviridae; Coronavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                 1112 IKWPWWVW 1119
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"Viral and cellular changes in a human cell line persistently
with human coronavirus HCOV-229E.";
with human coronavirus HCOV-229E.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF344187; AAK32189.1;
InterPro; IPR002551; Corona_S1.
InterPro; IPR002552; Corona_S2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1112 IKWPWWVW 1119
                                                                                                                                                                                                                                            Human coronavirus (strain 229E).
Viruses; ssRNA positive-strand viruses,
Coronaviridae; Coronavirus.
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                                                                                                                                                                                            STRAIN=229E;
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                                                                                                                                                                                 Bonavia A., Holmes K.V.;
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  2 LRWPWWPW 9
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                                                                                          STRAIN-BKL/0;
MEDLINE-9338943; PubMed-8397280;
Bridgen A., Duarte M., Tobler K., Laude H., Ackermann M.;
"Sequence determination of the nucleocapsid protein gene of
porcine epidemic diarrhoea virus confirms that this virus is
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01-NOV-1996
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Q84712;
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  STRAIN-BR1/87;
                   SEQUENCE FROM N.A
                                                           coronavirus related to human coronavirus transmissible gastroenteritis virus."; J. Gen. Virol. 74:1795-1804(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    porcine epidemic diarrhea virus Viruses; ssRNA positive-strand Coronaviridae; Coronavirus.
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Viruses; ssRNA positive-strand
Coronaviridae; Coronavirus.
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01-OCT-2001 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                  "Sequence of the spike
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                                                                                MEDLINE-98455678; PubMed-9782358; Bridgen A., Kocherhans R., Tobler K., Carvajal A., A "Further analysis of the genome of porcine epidemic Adv. Exp. Med. Biol. 440:781-786(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    coronavirus related to human coronavirus 229E and porcine transmissible gastroenteritis virus.";
J. Gen. Virol. 74:1795-1804(1993).
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    Kocherhans
                        SEQUENCE FROM STRAIN=CV777;
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                                                                                                                                                                                                                                "PEDV leader sequence and junction sites.", Adv. Exp. Med. Biol. 380:541-542(1995).
                                                                                                                                                                                                                                                                             Pobler K., Ackermann M.;
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Duarte M., Tobler K., Bridgen A.,
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Duarte M., Tobler K., Bridgen A.,
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1600; Corona_S1; 1.
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  Ackermann
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                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

KANG T.-J., Lim Y.-Y., Jang Y.-S., Kwon T.-H.,

"Spike Protein gene of Korea Porcine Epidemic

Submitted (APR-2002) to the EMBL/GenBank/DDBJ

EMBL; AF500215; AAM19716.1; -.

SEQUENCE 1386 AA; 151853 MW; 11F98BCB2AA05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8QQ98;
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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                   Puyesky M., Benhamou N., Ponce Noyola P., Bauw G., Van Montagu M., Herrera Estrella A., Horwitz B.A.; "Power M., Herrera Estrella A., Horwitz B.A.; "Power M., Herrera Estrella A., Horwitz B.A.; "Conidiospore surface protein of Trichoderma."; "Fungal Genet. Biol. 27,88-99(1999).
                                                                                     SEQUENCE FROM N.A. STRAIN-ATCC 32173;
                                                                                                                   Hypocreales; mit
NCBI_TaxID=5544;
                                                                                                                              Eukaryota; Fungi; Ascomycota;
Hypocreales; mitosporic Hypocr
                                                                                                                                                                         Conidiospore surface protein.
                                                                                                                                                                                     01-JUN-2002
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01-NOV-1999
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Coronaviridae; Coronavirus.
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InterPro; IPR002552; Corona_S2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          coronavirus
                                                                                                                                                      Trichoderma
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                                                                         MEDLINE=99343881; PubMed=10413618;
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les 5; Conserv
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AJ133651;
P01180; 1N
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62.5%;
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62.5%;
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RESULT 12
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Matches 5; Conserv
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Q8ZU59;
01-MAR-2002
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InterPro; IPR001673; S_mold_repeat.
ProDom; PD006869; S_mold_repeat; 2.
PROSITE; PS01346; CLAUDIN; UNKNOWN_1.
PROSITE; PS01346; CLAUDIN; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                      Pfam; PF0
Complete
             ....usunye w., wirkner U., Mewes H.W., Gassenhubk Submitted (JUN-1999) to the EMBL/GenBank/DDBJ EMBL; AL096753; CAB46428.2; -.
Hypothetical profice:
                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                Q9Y4N1 PRELIMINARY; PRT; 299. Q9Y4N1; Q9Y4N1; C1940N1; C1-2000 (TrEMBLrel. 12, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence 01-MAY-2000 (TrEMBLrel. 13, Last annotatine through the total 14.0 kDa protein (Fragment). DKFZP434C192.
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                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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STRAIN=IM2 / ATCC 51768 / DSM 7523.
PubMed=11792869;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thermoproteaceae; Pyrobaculum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pyrobaculum aerophilum.
Archaea; Crenarchaeota;
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Hypothetical
NON_TER
                                                                                                                      Homo sapiens (Human).
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Pfam; PF00809; Pterin_bind; 1.
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                                                       TISSUE=TESTIS;
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                                                                  SEQUENCE FROM N.A.
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298 AA;
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71.4%;
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Pred. No.
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Pred. No.
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                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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01-MAY-1997
01-JUN-2002
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., I Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yai Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thermoactinomyces vulgaris.
Bacteria; Firmicutes; Bacillus/Clostridium
Thermoactinomycetaceae; Thermoactinomyces.
                                                                                         STRAIN=C57BL/6J; TISSUE=EMBRYO; MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hofemeister J.W.;
Submitted (DEC-1996) to
EMBL; Z83214; CAB05671.
HSSP; P00800; 1HYT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001570; Peptidase, Pfam; PF01447; Peptidase_M4; 1 Pfam; PF02868; Peptidase_M4_C; SEQUENCE 504 AA; 56653 MW;
                                                                                                                                SEQUENCE
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Pred. No. 36;
2; Mismatches
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5A7BCC05C5AD1315 CRC64;
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                                                                       Kuit K.H., Rodriguez S., Santos
Shah R.S., Bahret A., Bal H.P.,
McCombie W.R.;
"Genomic Sequence For Oryza sati
Clone OSJNBA0058E19, Complete Se
Submitted (MAR-2001) to the EMBL
EMBL; A0083945, AAK13143.1; -.
Hypothetical protein.
SEQUENCE 327 AA; 36672 MW; :
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wynshaw-Boris A., Yoshida K., Hase Hayashizaki Y.;
"Functional annotation of a full-
Nature 409:685-690(2001).
EMBL; AK012846; BAB28508.1; -
MGD; MGI:1919917; 2810031J10Rik.
InterPro; IPR003309; Treg_SCAN.
Pfam; PF02023; SCAN; 1.
SMART; SM00431; LER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa (Rice).
Eukaryota; Viridiplantae; Stre
Spermatophyta; Magnoliophyta;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=4530;
                                                                                                                                           Spiegel L.A., King L., Kirchoff
Nascimento L.U., Vil M.D., Baker
Kuit K.H., Rodriguez S., Santos
Shah R.S., Bahret A., Bal H.P.,
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01-JUN-2001 (TrEMBLrel. 17,
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01-DEC-2001 (TrEMBLrel. 19,
Hypothetical 36.7 kDa protei
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Complete Sequence.";
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                                                                                                                                          Baker J.P., Miller B.
antos L., Zutavern T.,
H.P., O'Shaughnessy A.
                                   Score 50; DB; Pred. No. 33; O; Mismatches
                                    0;
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EMBL/GenBank/DDBJ
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Q94CI8
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Q8V7I1
Q9DUC9
Q98414
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O9duc4 tt virus. o
O91rd8 tt virus. o
O9dt80 tt virus. o
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O91d08 tt virus. o
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O90dvet tt virus. o
O8twg0 methanopyru
O94v618 lycopersico
O8v711 tt virus. o
O9duc9 tt virus. o
O9duc9 tt virus. o
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Q94ci8
Q8v7i1
Q9duc9
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ALIGNMENTS

Q9Y7V5 Q9Y7V5 AC Q9Y7V5; AC Q9Y7V5; PRELIMINARY; PRT; 1245 AA. AC Q9Y7V5; PT 01-W0V-1999 (TrEMBLrel. 12, Careated) DT 01-W0V-1999 (TrEMBLrel. 21, Last annotation update) DC (Conidiospore surface protein COPIC (CMP1. CMP1. CMP1. COPIC (CMP1. CMP1. CMP1. COPIC (CMP1. CMP1. CMP1.
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                     Virology 2/7:300-3/000-1000
EMBL; AB041959; BAB193131; -.
EMBL; AB041959; BAB193131; -.
InterPro; IPR001563; Serine_carbpept.
InterPro; IPR004219; TTvirus_Unk.
Pfam; PF02956; TT_ORF1; 1.
PROSITE; PS00131; CARBOXYPEPT_SER_SER; UNKNOWN_1.
PROSITE; PS00131; CARBOXYPEPT_SER_SER; UNKNOWN_1.
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EMBL; AB028669; BA94878.1; .
InterPro; IPR004219; TTVirus_Unk.
Pfam; PF02956; TT_ORF1; 1.
SEQUENCE 746 AA; 88561 MW; E01
                                                                                                                                                                 MEDLINE-20534983; PubMed=11080484; Okamoto H., Nishizawa T., Tawara A., Peng Y., Tal Kishimoto J., Tanaka T., Miyakawa Y., Mayumi M.; "Species-specific TT viruses in humans and nonhum phylogenetic relatedness."; Virology 277:368-378(2000).
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Okamoto H., Nishizawa T., Taw
Sai T., Sugai Y.;
"TT virus mRNAs detected in the
individual.";
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Pfam; PF02956; TT_OR
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Liu Z.H., Lu
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  MEDLINE-20568739; PubMed-11118348; Okamoto H., Nishizawa T., Tawara A Sai T., Sugai Y., Sugai Y., Tr virus mRNAs detected in the hor
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Kalman S., Mitchell W., Marathe R., Lammel C., Facilinger L., Grimwood J., Davis R.W., Stephens R.S "Comparative genomes of Chlamydia pneumoniae and
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CPN0426 OR CPJ0426 OR CP0327.
Chlamydia pneumoniae (Chlamydophila pneumoniae).
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Salzberg S.L.,
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01-JUN-2002
          D'Ambrosio E., Waitzkin S.D., Witney "Structure of the highly repeated, lo or LIRn) of the rat.";
Mol. Cell. Biol. 6:411-424(1986).
EMBL; M13100; AAA66046.1;
InterPro: IPRO00566; Lipocin_cytramp.
PROSITE; PS00213; LIPOCALIN; UNKNOWN_
                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
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Hypothetical 43.7 kDa protein.
Rattus norvegicus (Rat).
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EMBL; AB060592; BAB69900 l; -.
InterPro; IPR004219; TTvirus_Unk.
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                                                                                                                                                                                     TISSUE=LIVER;
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Eukaryota; Metazoa; Chordata;
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Yoshikawa A.;
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OBV7E2;

OBV7E2;

O1-MAR-2002 (TrEMBLrel. 2

O1-MAR-2002 (TrEMBLrel. 2

O1-JUN-2002 (TrEMBLrel. 2

ORF1 (Fragment).

TT virus.
                                            SEQUENCE FROM N.A.

STRAIN=AV19 / DSM 6324 / JCM 9639;

MEDLINE=21927647; PubMed=11930014;

Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N., Shekarbinina O.V., Shakhova V.V., Belova G.I., Aravind L., Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter I. Malykh A.G., Koonin E.V., Kozyavkin S.A.;

Malykh A.G., Koonin E.V., Kozyavkin S.A.;

"The complete genome of hyperthermophile Methanopyrus kandles and monophyly of archaeal methanogens.";

Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).

EMBL; AE010396; AAM02288.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  viremic infants.";
Arch. Virol. 147:21-41(2002).
EMBL; AB064615; BAB79374.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=21844401; PubMed=11855633;
MEDLINE=21844401; PubMed=11855633;
                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
NAD-dependent protein deacetylase, SIR2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Analysis of the complete genomes of thirteen \ensuremath{\text{TT}} virus classifiable into the fourth and fifth genetic groups,
                                                                                                                                                                                                                                                                                                                                                                                                                  NAD-dependent
SIR2 OR MK1075
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    Complete SEQUENCE
                                                                                                                                                                                                                                                                                                                                              Methanopyrus
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Archaea; Euryarchaeota;
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250 AA;
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Pred. No.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
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LEGRP1: A new member of glycine-rich proteins from tomato (Lycopersicon esculentum).";
Physiol. Plantarum 0:0-0(2001).

EMBL; AY026037; AAK08984.1; -.

EMBL; AY026037; AK08984.1; -.
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                                                                                                                "Analysis of the complete genomes classifiable into the fourth and viremic infants.",
Arch. Virol. 147:21-41(2002).
EMBL; AB064598; BAB79322.1;
InterPro; IPR004219; TTVirus_Unk.
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Pred. No. 19;

Mismatches

Indels

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Best Local Similarity
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Okamoto H., Nishizawa T., Tawara A., Peng
Kishimoto J., Tanaka T., Miyakawa Y., May
"Species-specific TT viruses in humans an
"hylogenetic relatedness.";
Virology 277:368-378(2000)
EMBL; AB041957; BAB19308.1;
Interpro; IPR004219; TTvirus_Unk.
Pfam; PF02956; TT_ORF1; 1.
SEQUENCE 735 AA; 86132 MW; 9ED818D6BE
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Q98414;
Q1-FEB-1997
Q1-FEB-1997
Q1-DEC-2001
                                                                                                                                                                                                                                          01-FEB-1997 (TrEMBLrel. 02, 01-FEB-1997 (TrEMBLrel. 02, 01-DEC-2001 (TrEMBLrel. 19, Envelope glycoprotein.
                                                                                                                                                                                        Ovine lentivirus.
Viruses; Retroid viruses;
NCBI_TaxID=11663;
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STRAIN-85/34; Carlson J.O., DeMartini J.C., Mwaengo D.M.; Envelope glycoprotein nucleotide sequence
                                                                   "Biological and genetic changes in ovine lentivirus strains passage in isogeneic twin lambs.";

Acquir. Immune Defic. Syndr. Hum. Retrovirol. 8:124-133(1
                                                                                                           MEDLINE=95135990; PubMed=7834396; Woodward T.M., Carlson J.O., de l DeMartini J.C.;
                                                                                                                                                  STRAIN-85/34;
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Pred. No. 19;
3; Mismatches
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Mayumi M.;
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                                                                                                                                        Transmembrane.
SEQUENCE 985 AA;
                                                                                                                                                               InterPro; IPR000328; Pfam; PF00517; GP41;
 223
                                              163 ILKRVYKQDWPWNTYHWPLWQMENMRQWMKENEREYKGRTNKTKEDIDDLLAGKIRGRFC 222
                       22
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VPYPFALLKCTKWCWYP
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Pred. No. 25;
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INDC_BUT
INDC_B AC 93046
DT 01-OCT
DC EWARMA
OC EWARMA
OC HOVIDA
RT SUE
RX MEDLIN
RA del Sa
RT CDNA
RI BIOCH
RX MEDLIN
RA CLILOZ
RT INDO
RT INDO
RT INDO
RT INDO
RT INDO
CC -1- FI
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CC -1- FI
CC -1- FI
CC OI SE
CC This I
CC OC ST

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01-OCT-1993
01-OCT-1993
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                     J. Biol.
                                                                                                                                                                                                                                                                                                                                                neutrophils.";
J. Biol. Chem.
                                                    Antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                        Cullor J.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus (Bovine).
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                                                                                                                                                                                                                                                                                                                                                                         "Indolicidin, a
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ALIGNMENTS

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PIR; JC1222; JC1222.
PIR; A42387; A42387.
InterPro; IPR001894; C
Pfam; PF00666; Catheli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE COMMUN. SEQUENCE COMMUN. 187:467-472(1992).

SEQUENCE COMMUN. RES. COMMUN. 187:467-472(1992).
SIGNAL
PROPEP
PEPTIDE
MOD_RES
                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                        InterPro; IPR001894; Cathelicidin.
Pfam; PF00666; Cathelicidins; 1.
Probom; PD001838; Cathelicidin, 1.
PROSITE; PS00946; CATHELICIDINS_1;
PROSITE; PS00947; CATHELICIDINS_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Ce
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Neutrophils;
MEDLINE=92165771; PubMed=1537821;
                                                                                                                                                                                                                                                                                                            EMBL; X67340; CAA47755.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Biol. Chem. 267:4292-4295(1992).

-i- FUNCTION: POTENT MICROBICIDAL ACTIVITY, ACTIVE AGAINST
-i- STAPHYLOCOCCUS AUREUS AND ESCHERICHIA COLI.

-i- TISSUE SPECIFICITY: LARGE GRANULES OF NEUTROPHILS.
-i- PTM: ELASTASE MIGHT BE RESPONSIBLE FOR ITS MATURATION.
-i- SIMILARITY: BELONGS TO THE CATHELLCIDIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Selsted M.E., Novotny M.J., Morris W.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indolicidin precursor.
                                                                                                     Amidation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      novel bactericidal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27, Created)27, Last sequence update)35, Last annotation update)
  29
130
143
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                                                                                                     Signal.
                             INDOLICIDIN
                                                                                POTENTIAL.
  PYRROLIDONE CARBOXYLIC ACID (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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POLG_EMCV
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Query Match
Best Local
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                                                                                     P03304;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-JUN-2002 (Rel. 41, Last annotation update)
19-JUN-2002 (Rel. 01, Last sequence update)
19-JUN-2002 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 35.7 kDa protein in mala 3'region
Bacillus stearothermophilus.
Bacteria; Firmicutes; Bacillales; Geobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q45633;
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Molecular cloning of a maltose transport gene from Bacillus stearothermophilus and its expression in Escherichia coli K-12."; Mol. Gen. Genet. 243:343-352(1994).
-!- SIMILARITY: BELONGS TO THE UPF0097 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein. SEQUENCE 314 AA; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=ATCC 7953;
MEDLINE=94247374; PubMed=8190087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN=ATCC 7953;
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Pfam; PF02834; 2_5_ligase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L13418; AAA71981.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1422;
                                         Encephalomyocarditis virus. Viruses: ssRNA positive-str
                                                                                                                                                                                                                                                                                     POLG_EMCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    liong E.C., Ferenci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 ELQSVILPWKWPWWPWRR 143
                                                                                                                                                                                                                                                                                                                                                                                                         222 LKQWQWEQAKARWEAERDADGARREPGETWDFLLDKPSWWERLIGRWRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 EAEPIMILKKWPWWPWRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 LKKWPWWPWRRKHEAEPEA----EP----IMILKKWPWWP-----WRR 36
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17; Conserv
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107
143
144 AA;
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                                            positive-strand viruses,
                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35735 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2_5_ligase.
igase; 2.
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BY SIMILARITY.
BY SIMILARITY.
ANIDATION (G-144 PROVIDE AMIDE GROUP).
E3B1CBBE55C09911 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 62; DB 1 Pred. No. 0.99; 5; Mismatches
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                                                 no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Length 314;
                                                 DNA
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                                                 stage;
                                                                                                                   RNA polymerase
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                                                      Picornaviridae
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                                                                                                                                                                    Core
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RESULT 4
MMLA_STRCO
ID MMLA_S'
AC Q53902
DT 30-MAY
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                                                                                                                                                      Query Match
Best Local S
                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The nucleotide and deduced amino acid sequences of the encephalomyocarditis viral polyprotein coding region.";
Nucleic Acids Res. 12:2969-2985(1984).

-i- FUNCTION: P3C POLYPEPTIDE IS A PROTEASE THAT CLEAVES AT CERTAIN
-i- FUNCTION: P3C POLYPEROTEIN. IT MAY BE A CYSTEINE PROTEASE.
-i- Q/G SITES IN THE POLYPROTEIN. IT MAY BE GIN-1-GIy bond in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                           ACT_SITE
ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=12104;
[1]
                                                                                                                                                                                                                                                                                                                                                                                            Polyprotein; Coat protein; Core protein; Transferase; RNA-directed RNA polymerase; Hydrolase; Thiol protease;
                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00073; rnv; 3.

Pfam; PF00680; RNA_dep_RNA_pol; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000605; RNA_helicase.
InterPro; IPR001205; RNA_pol_P3D.
InterPro; IPR001676; Rhv.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X00463; CAA25152.1;
                                                                                                                                                                                                                               LIPID
                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEROPS; C03.009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A03906
                                                                                         967
                                                                                                                 6 PWWPWRRKHEAEPEAEPI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      poliovirus polyprotein. In other picornavirus reactions Glu me
substituted for Gln, and Ser or Thr for Gly.
CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE I SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: THE VIRUS CAPSID IS EACH OF WHICH IS COMPOSED OF
                                                                                         PWNPWKNTYQAVLRAEPCRVTMDIYYKRVRPFRLPLVQKEWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P12296;
                                                                                                                                           | Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND VP4.
                                                                                                                                                                                                                                              623
911
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                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                     RNA_helicase;
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391
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910
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1192
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                                                                                                                                                        24.7%;
                                                                                                                                                                                               255756
                                                                                                                                                                                               WW;
                                                                                                                                                                                                                                                                                COAT PROTEIN VP1
CORE PROTEIN P2A
CORE PROTEIN P2B
CORE PROTEIN P2C
CORE PROTEIN P3A.
                                                                                                                                            6
                                                                                                                                                        Score
Pred.
                                                                                                                                                                                                                                             GENOME-LINKED PROTEIN VPG (H).
PICORNAIN 3C (P22).
RNA-DIRECTED RNA POLYMERASE P3D (E).
                                                                                                                                                                                                         PROTEASE (POTENTIAL).
PROTEASE (POTENTIAL).
                                                                                                                                                                                                                                   MYRISTATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                   LEADER PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ONE COPY
                                                                                                                                              Mismatches
                                                                                                                                                                                               26BC81BB7CF68CB5 CRC64;
                                                                                                                                                                                                                                                                                                                                              PROTEIN VP4 (RHO).
PROTEIN VP2 (BETA)
PROTEIN VP3 (GAMMA
                                                                                                                                                       No. 14;
                                                                                                                     -MILKKWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EACH O
                                                                                                                                                                       DΒ
                                                                                                                                                                                                                                                                                                                                               (BETA).
(GAMMA).
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                                                                                                                                                                                                                                                                                                                      (G).
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                                                                                                                                                                                                                                                                                                                                     (ALPHA)
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                                                                                             1008
                                                                                                                                                                    Length 2290;
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MMLA_STRCO Q53902; 30-MAY-2000

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-91347376; PubMed-1878971;
Fernandez-Moreno M.A., Caballero J.L., Hopwood D.A., Malpartida F.;
"The act cluster contains regulatory and antibiotic export genes, direct targets for translational control by the blda tRNA gene of Streptomyces.";
                                                                                                                                                                                             TRANSMEM
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[2]
                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genome sequence of the model actinomycete coelicolor A3(2)."; Nature 417:141-147(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=A3(2) / M145;
MEDLINE=21996410; PubMed=12000953;
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Streptomyces coelic
                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                       TIGREAMS; TIGRO0833; actII; PROSITE; PS50156; SSD; 2.
                                                                                                                                                                                                                                                                                                                            EMBL: AL593842; CAC44197.1; -.
InterPro; IPR004707; ACtII.
InterPro; IPR000731; HMGCR/patch_STM.
InterPro; IPR004869; MMPL.
                                                                                                                                                                                                                                                                                                                                                                     EMBL; M64683; AAA26691.1; -. EMBL; AL593842; CAC44197.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Actinomycetales;
NCBI_TaxID=1902;
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15-JUN-2002
332
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4 OR SCBAC28G1.10.
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47.4%;
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ENV_CAEVG

ID ENV_CAEVG

AC P31627;

DT 01-JUL-1993;

DT 16-OCT-2001

DT 16-OCT-2011

DE ENV POLYPIOTE

DE ENV POLYPIOTE

OS CAPTINE ARTH

OC VITUSES; Ret

OX NCBI_TaXID=1.

RN SEQUENCE FRO

RA KNOWLES D.P.

RA HATWOOD W.G..
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Matches
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SEQUENCE FROM N.A., A MEDLINE=92015464; Pul Knowles D.P. Jr., Che Harwood W.G., Stem T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genome.";
J. Mol. Evol.
-!- FUNCTION:
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TRANSMEM
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01-OCT-1996 (Rel.
15-JUN-2002 (Rel.
                                                           Caprine arthritis encephal Viruses; Retroid viruses; NCBI_TaxID=11662;
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MEDLINE=94047124; Pu
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16-OCT-2001 (Rel. 40, Last seg
16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00895; ATP-synt_8; Hydrogen ion transport; CF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- FUNCTION: THIS IS ONE OF THE CHAINS (CF(0) SUBUNIT) OF THE MITOCHONDRIAL -i- CATALYTIC ACTIVITY: ATP + H(2)O + H(4)
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NCBI_TaxID=8839;
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-!- SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.
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een the Swiss Institute of Bioinformatics and the EM
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Bioinformatics Institute.
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(Rel. 41, Last annotation
protein 8 (EC 3.6.3.14)
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             PubMed=1656067;
Cheevers W.P.,
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PubMed=8230253;
                                                                                       encephalitis
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                                       AND
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rsor (Coat polyprotein)
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                                                                           litis virus (s
Retroviridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Structure and genetic variability of envelope glycoproteins of two antigenic variants of caprine arthritis-encephalitis lentivirus."; J. Virol. 65:5744-5750(1991).
      ENV_OMVVS
P16899;
01-AUG-1990
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CARBOHYD
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                            STANDARD;
       15,
15,
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       Last sequence update)
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; Pred. No. 18;
7; Mismatches
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TRANSMEMBRANE PROTEIN (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC
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Query Match
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Matches 14
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PIR; G46335; G46335.
HIV; M34193; ENV$OMVVSACG.
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Querat G., Audoly G., Sonigo P., '
"Nucleotide sequence analysis of '
lentivirus: phylogenetic history of Virology 175:434-447(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ovine lentivirus
Viruses; Retroid
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Pfam; PF00517;
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lysis of SA-OMVV, a visna-r.
history of lentiviruses.";
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Retroviridae; Lentivirus
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harr.
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Batcan J., Moule S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
Nature 393:537-544(1998).
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01-OCT-1996 (Rel. 34, Last sequence
15-JUN-2002 (Rel. 41, Last annotat.
Hypothetical protein Rv1355c
RV1355C OR MT1398 OR MTCY02B10.19C
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EMBL; AE007012; AAK45661.1;
TIGR; MT1398; -
TubercuList; Rv1355c; -
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STRAIN=CDC 1551 / Oshkosh;
                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein; Complete proteome. SEQUENCE 715 AA; 78181 MW; 455495248A56041C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Peterson J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Belcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
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01-OCT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Actinomycetales;
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Capteels-3223697; PubMed-8467807;
Casteels-Josson K., Capaci T., Casteels P., Tempst
Casteels-Josson M., Capaci T., Casteels P., Tempst
Papidaecin multipeptide precursor structure: a puta
amplification of the insect antibacterial response.
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                                                         Cysteinyl-tRNA
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Casteels P., Ampe C., Jacobs F., Vaeck M., Tempst P. Apidaecins: antibacterial peptides from honeybees. EMBO J. 8:3387-3391(1989).
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Insecta; Pterygota; Neoptera; Endopterygota;
Aculeata; Apodea; Apidae; Apis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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Pfam; PF01406; tRNA-synt_le; 1.
PRINTS; PR00983; TRNASYNTHCYS.
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PROSITE; PS00178; AA_TRNA_LIGASE_I;
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Cysteinyl-trnA synthetase 1 (EC 6.1.1.16) (Cysteine--trnA ligase (CysRS 1).
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PROSITE; PS00178; AA_TRNA_LIGASE_I; FALSE_NEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002308; Cys_tRNA-synt_1a
InterPro; IPR001412; tRNA-synt_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AL583918; CAC29831.1;
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-!- CATALYTIC ACTIVITY: ATP + L-cysteine +
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SUBUNIT: MONOMER (BY SIMILARITY).
SUBCELLULAR LOCATION: CYCOPIasmic.
SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
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                                                                                                                                                                                                                                                                               PWWPWRRKHE---
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473 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 1- SUBCELLULAR LOCATION: Type I membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Raabe T., Schelle-Prinz B., Siddell S.G.;
"Nucleotide sequence of the gene encoding thuman coronavirus HCV 229E";
J. Gen. Virol. 71:1065-1073(190).
-i- FUNCTION: THE PEPLOMER PROTEIN MEDIATES
TO THE HOST CELL RECEPTOR AND IS INVOLVE
AND IN SYNCYTIUM FORMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=90264837;
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Coronaviridae; Co
NCBI_TaxID=11137;
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 Similarity
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IPR002552; Corona_S2.
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EXTRACELLULAR (POTENTIAL).
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DC Q9YSO5; Q9UHY2;
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DT 15-JUN-2002 (Rel. 41, Last annotation updated)
DT 15-JUN-2002 (Rel. 41, Last annotation updated)
DT 15-JUN-2002 (Rel. 41, Last annotation updated)
DT 16-CCT-2001 (Rel. 40, Last sequence updated)
DE Attial natrituteria;
PR SEQUENCE PROM N.A.
RC TISSUE-Heart;
RY MEDLINE-99262666; PubMed=10329693; RA Yan W., Wall-Sequence updated u
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Proc. Natl. Acad. Sci. U.S.A. 97:8525-8529(2000)
-i- FUNCTION: CONVERTS PRO-ANP TO ANP. CLEAVES P
BETWEEN ARG-123 AND SER-124.
-i- SUBCELLULAR LOCATION: Type II membrane prote
-i- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEAR
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                                                                                                                                                                                                                                                                                                                     between the Swiss Institute of Bioinformathe European Bioinformatics Institute. The by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Corin, a transmembrane cardiac serine protease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO PEPTIDASE FAMI
SIMILARITY: CONTAINS 7 LDL-RECEPTOR C
SIMILARITY: CONTAINS 7 FRIZZIED (FZ)
SIMILARITY: CONTAINS 1 SRCR DOMAIN.
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                                                                                                                                                                                                                                                                         equires a license agreement (Semail to license@isb-sib.ch).
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LDL-RECEPTOR CLASS A
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Catarrhini;
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ting enzyme (EC 3.4.21.-)
specific serine proteinas
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i; Hominidae;
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ne serine protease
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N HEART.
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SEQUENCE
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CONFLICT
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 813 WPWQCSLQSEPSGHICGCVLIAKKW 837
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; PF01392;
                     WPWRRKHEAEPEAE---PIMILKKW 29
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SM00202; SR; 1.
SM00020; Tryp_SPC; 1.
E; PS50038; FZ; 2.
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PS50240;
PS00134;
PS00135;
                                                Similarity 9; Conserv
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1022
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• 854
• 116564 MW;
72.28;
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SRCR_2; FALSE_NEG.
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TRYPSIN_HIS; FALSE_NEG.
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66
                                                               22.2%;
36.0%;
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                                                                                                                                        N-LINKED (GLCNAC...) ()
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CHARGE RELAY SYSTEM (
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
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                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                             Score 53.5;
Pred. No. 36
                                                                                                                                                                                                                                                                                                                                                                          N-LINKED
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                                                                                                                                                                                                                                                                                   N-LINKED
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                                                                                                     W -> R (IN REF. 2).
K -> R (IN REF. 2).
MW; 7705398EBB607AD2 CRC64;
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LDL-RECEPTOR CLASS
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                                                                   36;
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(BY
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SIMILARITY).
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CORI_MOUSE
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PRINTS; PRO0261; LDLRECEPTOR.
SMART; SM00063; FRI; 2.
SMART; SM000702; LDLa; 7.
SMART; SM00202; SR; 1.
SMART; SM00202; SR; 1.
SMART; SM00202; Tryp_SPC; 1.
PROSITE; PS50038; FZ; 2.
PROSITE; PS50038; FZ; 2.
PROSITE; PS50068; LDLRA_1; 6.
PROSITE; PS50068; LDLRA_2; 7.
PROSITE; PS500420; SRCR_1; FALSE
PROSITE; PS500420; SRCR_1; FALSE
                                                                                                                                                                                                                                                                                                                                 Pfam; Provos
Pfam; PF00089; tryp-
Pfam; PF01392; Fz;
PFam; PF01392; CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Atrial natriuteric peptide-converting enzyme (EC 3.4.21.-) (pro-ANP-converting enzyme) (Corin) (Low density lipoprotein receptor related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORI_MOUSE Q9Z319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. BIOCHEM. 124.784.789(1998).

J. BIOCHEM. 124.784.789(1998).

I. FUNCTION: CONVERTS PRO-ANP TO ANP. CLEAVES PRO-ANP S. BETWEEN ARG-122 AND SER-123 (BY SIMILARITY).

SUBCELLULIAR LOCATION: Type II membrane protein.

I. TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART.

I. SIMILARITY: DELONGS TO PEPTIDASE FAMILY S1.

I. SIMILARITY: CONTAINS 7 LDL-RECEPTOR CLASS A DOMAINS.

I. SIMILARITY: CONTAINS 2 FRIZZLED (FZ) DOMAINS.

I. SIMILARITY: CONTAINS 1 SRCR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         membrane protein-like structure is abundant in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-98429596; PubMed=9756624;

MEDLINE-98429596; PubMed=9756624;

Tomita Y., Kim D.-H., Magoori K., Fujino T., Yamamoto T.T.;

"A novel low-density lipoprotein receptor-related protein with
"A novel low-density lipoprotein abundant in heart.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRN OR LRP4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein 4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
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DOMAIN
DOMAIN
                                                                                                                                         PROSITE; PS00420; SRCR_1; FALSE_NEG. PROSITE; PS50287; SRCR_2; 1. PROSITE; PS50240; TRYPSIN_DOM; 1. PROSITE; PS00134; TRYPSIN_HIS; FALSE
                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001314; Chymotrypsin.
InterPro; IPR000024; Fz_domain.
InterPro; IPR002172; LDL_recept_A.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001190; Srcr_receptor.
pfam; PF00057; ldl_recept_a; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AB013874;
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                                                                            Glycoprotein; Repeat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P00763;
                                                             TRANSMEM
                                                                                                           Hydrolase;
                                                                                                                              PROSITE; PS00135;
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trypsin; 1.
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      1113
327
372
                                                                                                           protease;
                                                                                                                              TRYPSIN_HIS; TRYPSIN_SER;
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Rodentia;
                                                               112
133
                                                CYTOPLASMIC (POSIGNAL-ANCHOR (POTENTIAL).
                                                                                                               Transmembrane; Signal-anchor;
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                  EXTRACELLULAR FZ 1.
      LDL-RECEPTOR CLASS A 1
                                                                                                                                 FALSE_NEG
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"Cloning of a higher-plant plastid omega-6 fatty acid desaturase cDNA and its expression in a cyanobacterium."; plant physiol. 105:635-641(1994).

-i- FUNCTION: CHLOROPLAST OMEGA-6 FATTY ACID DESATURASE INTRODUCES THE SECOND DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
-i- PATHWAY: POlyunsaturated fatty acid biosynthesis.
                                                                                                                                                                                                                                    Glycine max (Soybean).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Rosid: Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid: spermatophyta; Magnoliophyta; Papaleos; Papilionoideae; Phaseoleae; Glycine eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine
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InterPro; IPR001225; FA_desaturase.
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Qy 19 EAEPIMILKKWPWWPWRR 36 : ::: Db 126 ELQSVILPWKWPWWPWRR 143	Query Match 32.4%; Score 78; DB 1; Length 144; Best Local Similarity 55.6%; Pred. No. 0.011; Matches 10; Conservative 4; Mismatches 4; Indels 0; Gaps 0;	RESULT 1 JC1222 JC1222 Indolicidin precursor - bovine N;Alternate names: antimicrobial peptide C;Species: Bos primigenius taurus (cattle) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C;Accession: JC1222; A42387; S25664 R;Gel Sal, G; Storici, P; Schneider, C; Romeo, D; Zanetti, M. Blochem. Blophys. Res. Commun. 187, 467-472, 1992 A;Title: CDNA cloning of the neutrophil bactericidal peptide indolicidin. A;Reference number: JC1222; MUID:92392368; PMID:152037 A;Accession: JC1222; MUID:92392368; PMID:152037 A;Molecule type: mRNA A;Residues: 1-144 <sal> A;Cross: references: EMBL:X67340; NID:9462; PIDN:CAA47755.1; PID:9463 A;Experimental source: bone marrow R;Selsted, M.E.; Novotny, M.J.; Morris, W.L.; Tang, Y.Q.; Smith, W.; Cullor, J.S J. Biol. Chem. 267, 4292-4295, 1992 A;Title: Indolicidin, a novel bactericidal tridecapeptide amide from neutrophils A;Accession: A42387; MUID:92165771; PMID:1537821 A;Accession: A42387; MUID:92165771; PMID:1537821 A;Residues: 131-143 <sel> A;Experimental source: neutrophils A;Residues: 131-143 <sel> A;Rote: sequence extracted from NCBI backbone (NCBIP:83840) C;Superfamily: cathelin; cystatin homology C;Keyords: amidated carboxyl end F;12-2/Domain: cystatin homology C;Superimental cystatin homology C;Morrimental cystati</sel></sel></sal>	ALIGNMENTS	30 53.5 22.2 538 2 B84759 hypothetical prote 31 53.5 22.2 113 2 JE0315 low-density lipopr 32 53 22.0 68 2 E88799 hypothetical prote 23 53 22.0 406 2 H69143 comega-6 desaturase 23 53 22.0 424 2 T07742 comega-6 desaturase 23 53 22.0 480 2 JC7752 shb-like adapter pote 23 22.0 24 2 JC7752 shb-like adapter pote 24 25 25 21.8 42 2 JC7552 capsid polyprotein 39 52.5 21.8 2292 2 S35961 H+-transporting two 25 25 21.8 471 2 T50016 transcription fact 42 52.5 21.8 471 2 T50016 transcription fact 44 52.5 21.8 490 2 T21365 hypothetical prote 25 25 21.8 490 2 T21365 hypothetical prote 25 25 21.8 51 2 T39589 hypothetical prote 25 25 21.8 51 2 T39589 hypothetical prote 25 25 21.8 490 2 T21365 hypothetical prote 25 25 21.8 51 2 T39589 hypothetical prote 25 25 25 21.8 51 2 T39589 hypothetical prote 25 25 25 21.8 51 2 T39589 hypothetical prote 25 25 25 21.8 51 2 T39589 hypothetical prote 25 25 25 21.8 51 2 T39589 hypothetical prote 25 25 25 21.8 51 2 T39589 hypothetical prote 25 25 25 21.8 51 2 T39589 hypothetical prote 25 25 25 21.8 51 2 T39589 hypothetical prote 25 25 25 21.8 51 2 T39589 hypothetical prote 25 25 25 21.8 51 2 T39589 hypothetical prote 25 25 25 21 2 T39589 hypothetical prote 25 25 25 25 25 25 25 25 25 25 25 25 25
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F.; Ouchi, K.; Shiba,

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RESULT H86543

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C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
C;Accession: D72081; G81589
R;Kalman, S; Mitchell, W; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; (Nature Genet, 21, 385-389, 1999)
                                                                                                                                                                                                           hypothetical protein 3 - Bacillus stearothermophilus
(;Speciles: Bacillus stearothermophilus
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 15-Oct-1999
C;Accession: S43916
R;Liong, E.C.; Ferenci, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Experimental source: strain CWL029
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzber Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: G81589
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-192 <STO>
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A;Experimental source: strain AR39, HL cells
C;Genetics:
A;Gene: CPn0426; CP0327
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A;Residues: 1-192 <ARN>
A;Cross-references: GB:AE001625; GB:AE001363; NID:g4376695; PIDN:AAD18570.1; PID:g437670
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                    A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-314 <LIO>
A;Cross-references: EMBJ
                                                                                                                   A; Title: Molecular cloning of a maltose transport gene from A; Reference number: S43914; MUID:94247374; PMID:8190087 A; Accession: S43916
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A; Residues: 1-192 < REA>
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243, 343-352, 1994
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EMBL:L13418; NID:g436964; translated the initiation
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42.3%;
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42.3%;
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Pred. No.
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Pred. No. 1;
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PIDN:AAA71981.1; PID:g436967 codon GTG for residue 1 as Val
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Salzberg,
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                         genome polyprotein - encephalomyocarditis virus N;Contains: coat protein VP1; coat protein VP2; coat EC 3.4.-.); RNA-directed RNA polymerase (EC 2.7.7.48 C;Species: encephalomyocarditis virus, EMCV
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hypothetical protein CC1782 [imported] - Caulobacter crescentus C;Species: Caulobacter crescentus C;Species: Caulobacter crescentus C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001 C;Accession: B87470
                                                                                                                                                                                                                                                                                                             hypothetical protein SCE36.09 - Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 C; Accession: T36208 C; Accession: T36208 R; Oliver, K; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajanc submitted to the EMBL Data Library, May 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AE005673; NID:g13423210; PIDN:AAK23758.1; GSPDB:GN00148 C;Genetics: A;Gene: CC1782
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A;Molecule type: DNA
A;Residues: 1-381 <STO>
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"hehes 17; Conserv
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A; Residues: 1-114 <OLI>
A; Cross-references: EMB
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A; Accession: T36208
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93
                                                                                        Local Similarity
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PETAPADAARRWRPRWPWRR 112
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ce: strain A3(2)
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Pred. No.
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Pred.
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                                                                                                                                                                                                                                                                                                               S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, May 1999
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host Homo

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Jac protein 7.48)

VP3;

coat

protein

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A; Gene:
A; Map po
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A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: E86447
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A;Accession: JN0383
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R;Palmenberg, A.C.; Kirby, E.M.; Janda, M.R.; Drake, N.L.; Duke, Nucleic Acids Res. 12, 2369-2385, 1984
                                                                                                                                                                                                                                                                                                                               C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-95 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein F5D14.5 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar_2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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A; Residues: 1337-1396, 'L', 1398-1517, 'A', 1519-1536, 'E', 1538-1556, 'S', 1558-1611, 'T', 1613-A; Residues: GB: M44935
A; Note: the authors translated the codon CAU for residue 713 as Thr and AAC for residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:X00463; NID:g61034; PIDN:CAA25152.1; PID:g61035 R;Petrov, N.A.; Chizhikov, V.E.; Blinov, V.M.; Karginov, V.A.; Mikryukov, N.N.; Gutorov Bloorg. Khim. 10, 274-279, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: The nucleotide and deduced amino acid sequences A;Reference number: A03906; MUID:84169586; PMID:6324136
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A; Residues: 1-2290 <PAL>
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26.2%;
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           Score 59; DB
Pred. No. 1.6;
5; Mismatches
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Pred. No. 38;
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C:Species: Rattus norvegicus (Norway rat) (C;Date: 19-Mar-1997 #sequence_revision 17 C;Accession: S21976 R:Kahre, O.; Ilves, H.; Speek, M.

17-oct-1997

#text_change

26-Aug-1999

2.7.7.49)

(clone

MH2C)

rat retrotransposon

probable RNA-directed DNA polymerase (EC N; Alternate names: reverse transcriptase

S21976

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79

RKWPWSKPERPSAAEPDATP

98

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A; Reference number: S16783 A; Accession: S21976

submitted to the EMBL Data

Library,

August 1991

A; Molecule type:

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DNA Res.
A; Title:
                                                                                                                                                                                                                                                       hypothetical protein SC6G9.38 - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-485 <KAN>
A; Cross-references: EMBL:D90901;
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A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequ
C:Accession: S74708
Qγ
                                                                                    A; Gene:
                                                                                                   A; Experimental source: strain C; Genetics:
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A; Residues: 1-107 <SEE>
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                                                                                                                                                                                      A; Reference number: 221584
A; Accession: T35634
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Title commons
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12; Conser
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                               Conservative
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be: strain A3(2)
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was submitted
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Pred.
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Pred. No. 8.6;
                                                                                                                                PIDN:CAB45629.1;
                                                                                                                                                                                                                 K.D.; Parkhill,
June 1999
                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                               Mismatches
                                           No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -PVLVITDVGGEWSWWWW
                                             N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the unicellular cyanobacterium Synechocys
                                        2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NID:g1651897; PIDN:BAA16859.1; to the EMBL Data Library, June
                                                                                                                                                                                                                                                                                                                                                                                                                                                  2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 485;
                                                                                                                                GSPDB:GN00070;
                                                                                                                                                                                                                                                                                                                                                                18
                                                                                                                                                                                                                                                                                                                                                                                          28
                                                         Length
                               Indels
                                                                                                                                                                                                                                Barrell,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCC
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                                                                                                                                                                                                                                в.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                      18;
                            0;
                                                                                                                                SCOEDB: SC6G9.38
                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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1996
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A; Residues: 1-513 <KAH>.
A; Cross-references: EMBL: X61295;
A; Experimental source: clone MH2C C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein SPBC646.15c - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Mar-2000 C;Accession: T40591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Superfamily: pol polyprotein
C;Keywords: nucleotidyltransferase; polyprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-376 <SEE>
A;Cross-references: EMBL:AL035216; PIDN:CAA22819.1; GSPDB:GN00067; SPDB:SPBC646.15c
A;Experimental source: strain 972h-; cosmid c646
C;Genetics: C;Geneti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Mobile element: retrotransposon L1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Reference number: Z21938
A;Accession: T40591
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
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RESULT 14
T28094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cell 66, 769-780, 1991
A;Title: The abt cluster contains regulatory and antibiotic export genes, direct targets A:Reference number: A40046; MUID:91347376; PMID:1878971
A;Accession: C40046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibiotic transport-associated protein actII-3 - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 22-Oct-19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Map position: 2
A; Introns: 49/1; 126/2; 312/2; 350/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, submitted to the EMBL Data Library, January 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Вþ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                             Ъ
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                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-711 <FER>
A;Cross-references: GB:M64683; NID:g153143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Fernandez-Moreno, M.A.; Caballero,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Accession: C40046
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                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      236 WHWKRKQKSSS-----LKVRPWGPW 255
                                                                                                                                    332 IFGRWVFWPARPKHGTEPD 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           госат
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                                                                                                                                                                                          1 ILKKWPWWPWRRKHEAEPE 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23.9%;
l Similarity 37.0%;
10; Conservative
                                                                                                                                                                                                                                                           Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces pombe hypothetical protein SPBC646.15c
                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.18;
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Pred. No.
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Pred. No. 1
                                                                                                                                                                                                                                                                                                Score 57;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J.L.; Hopwood, D.A.;
                                                                                                                                                                                                                                                                     Mismatches
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12;
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                                                                                                                                                                                                                                                                                                                                                                                               PIDN:AAA26691.1; PID:g153146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                                                                                                                               DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
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Search completed: January Job time: 21 secs

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18:09:54

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hypothetical protein ZK899.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C:Accession: T28094
                                                                                                                                                                                                                                                                                                                                                                                             myosin heavy chain - fluke (Schistosoma mansoni) (fragment)
N;Alternate names: surface antigen, 200K
C;Species: Schistosoma mansoni
C;Species: Schistosoma mansoni
C;Date: 22-Nov-1993 #sequence_revision 06-Sep-1996 #text_change 13-Feb-1998
C;Accession: S33068
                                                                                                                                                                                                                                                                                                              R;Soisson, L.M.A.; Masterson, C.P.; Tom, T.D.; McNally, M.T.; Lowell, G.H.; Strand, M. J. Immunol. 149, 3612-3620, 1992
A;Title: Induction of protective immunity in mice using a 62-kDa recombinant fragment A;Title: Induction of protective immunity in Mice using a 62-kDa recombinant fragment A;Reference number: A46514; MUID:93056536; PMID:1431131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Introns: 34/3; 143/2; 227/2; 262/3; C; Superfamily: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Map position: X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:Z37140; PIDN:CAA85502.1; GSPDB:GN00028; CESP:ZK899.2 A;Experimental source: clone ZK899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-452 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: Z20468
A; Accession: T28094
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Kershaw,
                                                                                                                                                                  A;Cross-references: EMBL:X65591
A;Note: the authors translated the
C;Superfamily: myosin heavy chain;
C;Keywords: ATP; surface antigen
                                       δÃ
                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-527 <SOI>
В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Best Local S
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  106 VLRNWPWWRLYTKVKPMLNIARQEEEMKKAAEELAKLKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
les 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 KWPWWPWRRKHEAEPEAEPIMILKKWPWWPW 34
                                       1 ILKKWPWW-----PW----RRKHEAEPEAEPIMILKK
                                                                                   12;
                                                                                                       Similarity
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nilarity 32.3%;
Conservative
                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                              Masterson, C.P.; Tom, T.D.; McNally, M.T.; Lowell, G.H.;
                                                                                                       23.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Library,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 56;
Pred. No.
                                                                                                         Score 55.5;
Pred. No. 25;
                                                                                                                                                                                        codon CAA for residue 346 as myosin motor domain homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               September 1994
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hypothetical
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19;
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                                                                                       9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 452;
                                                                                                                            Length 527;
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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1: /cgn2_6/ptodata/1/pubpaa/Pi
2: /cgn2_6/ptodata/1/pubpaa/Pi
3: /cgn2_6/ptodata/1/pubpaa/Ui
4: /cgn2_6/ptodata/1/pubpaa/Ui
6: /cgn2_6/ptodata/1/pubpaa/Ui
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                    Query
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/cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
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 US-09-030-619-104
US-09-030-619-50
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US-09-030-619-17
US-09-030-619-17
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US-09-030-619-53
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(without alignments)
66.864 Million cell updates/sec
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Sequence
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69, Appl
52, Appl
51, Appl
99, Appl
108, Appl
110, Appl
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73	73	73.5	73.5	75	75	75	76	77	77.5	78	78	78	81	81	82	82	82	82	82.5	83	83	83	83	83.5	85
30.3	30.3	30.5	30.5	31.1	31.1	31.1	•	32.0		32.4	32.4	32.4	33.6		34.0		34.0	34.0	34.2	34.4	34.4	34.4	34.4	34.6	35.3
10	9	12	12	12	12	12	12	12	12	12	11	11	11	11	13	13	13	13	21	20	13	13	12	15	13
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US-09-030-619-81	US-09-030-619-80	030	us-09-030-619-75	US-09-030-619-111	03	US-09-030-619-23	-09-03	<u>.</u>	030-619-	-09-030	030	US-09-030-619-78	US-09-030-619-114	US-09-030-619-79	-03	US-09-030-619-94	US-09-030-619-59	us-09-030-619-58	US-09-030-619-48	US-09-030-619-24	us-09-030-619-106	US-09-030-619-105	US-09-030-619-44	us-09-030-619-39	US-09-030-619-103
Sequence 81, Appl		76,	⋗	Sequence 111, App	Sequence 30, Appl	23,		42,	40,		113,	78,	•	79,	102,	94,		58,	48,	24,	106,	105,		Sequence 39, Appl	Sequence 103, App

ALIGNMENTS

RESULT 1 US-09-030-619-104

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APPLICANT: Krieger, Timothy J.

APPLICANT: Taylor, Robert
APPLICANT: Erfle, Douglas
APPLICANT: Fraser, Janet R.
APPLICANT: West, Michael H.P.
APPLICANT: MITH ANTIBIOTICS
FILE REFERENCE: 660081.406
CURRENT APPLICATION NUMBER: US/09/030,619B
CURRENT FILING DATE: 1998-02-25
NUMBER OF SED ID NOS: 232
NUMBER OF SED ID NOS: 232
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                   RESULT 2
US-09-030-619-50
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               Sequence 50, Application US/09030619B Patent No. US20020035061A1 GENERAL INFORMATION:
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  APPLICANT:
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
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20; Conser
Krieger, Timothy J.
                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                               58.7%;
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                                                                                    RESULT 4
US-09-030-619-52
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; OTHER INFORMATION: Indolicidin Analogue
US-09-030-619-69
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LENGTH: 21
TYPE: PRT
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CURRENT APPLICATION NUMBER: US/09/030,619B
CURRENT FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 232
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 50
LENGTH: 28
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Best Local Similarity 64.3
Them 18; Conservative
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                            Sequence 52, Application US/09030619B Patent No. US20020035061A1 GENERAL INFORMATION:
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APPLICANT:
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APPLICANT:
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APPLICANT: West, Michael H.P.
APPLICANT: West, Michael H.P.
APPLICANT: West, Michael H.P.
APPLICANT: MICHAEL G. APPLICANT MESTICAL FOR TOWN MICHAEL GRAPH MICHAEL GENERAL GRAPH ANTIBOTICS
FILE REFERENCE: 660081.406
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CURRENT FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 232
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: West, Michael H.P.
APPLICANT: MCNICO1, Patricia J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
TITLE OF INVENTION: WITH ANTIBIOTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE:
APPLICANT:
                  APPLICANT:
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21; Conserv
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Erfle, Douglas
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Erfle, Douglas
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61.8%;
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64.3%;
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-MIL-RWPWWPWRRK 25
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Pred. No. 1.9e-10;
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Pred. No. 4.7e-06;
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                                                                   RESULT 6
US-09-030-619-95
; Sequence 95, Application U;
; Patent No. US20020035061A1
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SEQ ID NO 52
LENGTH: 21
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SEQ ID NO 51
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local 9
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APPLICANT: Fraser, Janet R.
APPLICANT: West, Michael H.P.
APPLICANT: West, Michael H.P.
APPLICANT: MCNicol, Patricia J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALC
TITLE OF INVENTION: WITH ANTIBIOTICS
FILE REFERENCE: 660081.406
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/030,619B
CURRENT FILING DATE: 1998-02-25
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                     Matches
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Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: West, Michael H.P.
APPLICANT: McNicol, Patricia J.
APPLICANT: McNicol, Patricia J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
TITLE OF INVENTION: WITH ANTIBIOTICS
FILE REFERENCE: 660081.406
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o. US20020035061A1
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Erfle, Douglas
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Krieger, Timothy J.
Taylor, Robert
Erfle, Douglas
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Pred. No. 6.1e-06;
Mismatches
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Pred. No. 2
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US-09-030-619-72
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US-09-030-619-99
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                                                               GENERAL INFORMATION:
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SEQ ID NO 95
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
          APPLICANT:
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APPLICANT:
                                                                               Sequence 72, Application US/09030619B Patent No. US20020035061A1
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Best Local :
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APPLICANT: West, Michael H.P.
APPLICANT: MCNICOL, Patricia J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: WITH ANTIBIOTICS
FILE REFERENCE: 660081.406
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CURRENT FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 232
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
TITLE OF INVENTION: WITH ANTIBIOTICS
FILE REFERENCE: 660081.406
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SOFTWARE: FastSEQ for Windows Version
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APPLICANT:
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TYPE: PRT
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          Krieger, Timothy J.
Taylor, Robert
Erfle, Douglas
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Erfle, Douglas
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100.0%; F1
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Pred. No.
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GENERAL INFORMATION: APPLICANT: Krieger

APPLICANT: APPLICANT: APPLICANT:

> Krieger, Timothy J. Taylor, Robert Erfle, Douglas

Fraser, Janet R. West, Michael H.P.

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CURRENT APPLICATION NUMBER: US/09/030,619B
CURRENT FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 232
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 108
LENGTH: 14
RESULT 10
US-09-030-619-47
Sequence 47, Application US/09030619B
; Patent No. US20020035061A1
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; OTHER INFORMATION:
US-09-030-619-72
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LENGTH: 14
TYPE: PRT
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APPLICANT:
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CURRENT FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 232
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT:
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TITLE OF INVENTION: COMPOSITIONS AND
TITLE OF INVENTION: INFECTIONS USING
TITLE OF INVENTION: WITH ANTIBIOTICS
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Erfle, Douglas
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Pred. No.
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. 2.7e-05;
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2.7e-05;
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RESULT 12
US-09-030-619-112
; Sequence 112, Application US/09030619B
; Patent No. US20020035061A1
; GENERAL INFORMATION:
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CURRENT FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 47
LENGTH: 21
TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 12; Conservative
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SOFTWARE: FastSEQ for
SEQ ID NO 67
LENGTH: 12
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APPLICANT: McNicol, Patricia J.
APPLICANT: MCNIcol, Patricia J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
TITLE OF INVENTION: WITH ANTIBIOTICS
TITLE OF INVENTION: WITH ANTIBIOTICS
TITLE OF TREFERENCE: 660081.406
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TITLE OF INVENTION: COMPOSI
TITLE OF INVENTION: INFECTI
TITLE OF INVENTION: WITH AN
FILE REFERENCE: 660081.406
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Erfle, Douglas
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              Fraser, Janet R. West, Michael H.P.
                                                   Taylor, Robert
Erfle, Douglas
                                                                                  Krieger, Timothy J
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COMPOSITIONS AND METHODS FOR TREATING INVECTIONS USING CATIONIC PEPTIDES ALG WITH ANTIBIOTICS
 Patricia J
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                                                                                                                                                                                                                                                                                                                  Score 87; DB 10; Pred. No. 6.7e-05;
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Pred. No. 0.0001;
1; Mismatches 0;
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; OTHER INFORMATION: Indolicidin Analogue
US-09-030-619-53
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SEQ ID NO 112
LENGTH: 12
TYPE: PRT
                                                                                                                                                              US-09-030-619-107
                                                                                              GENERAL INFORMATION: APPLICANT: Krieger,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                               Sequence 107, Application US/09030619B Patent No. US20020035061A1
                                                                                                                                                                                                                                                                                                         Query Match
Best Local
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APPLICANT:
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TITLE OF INVENTION: INFECTIONS USING CATIC
TITLE OF INVENTION: WITH ANTIBIOTICS
FILE REFERENCE: 660081.406
CURRENT APPLICATION NUMBER: US/09/030,619B
CURRENT FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 232
                                                                                                                                                                                                                                                                                            Matches
                                                               APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/030,619B CURRENT FILING DATE: 1998-02-25 NUMBER OF SEQ ID NOS: 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Fraser, Janet R.
APPLICANT: West, Michael H.P.
APPLICANT: MCNICOL, PARTICIA J.
TITLE OF INVENTION: COMPOSITIONS AND
TITLE OF INVENTION: INFECTIONS USING
TITLE OF INVENTION: WITH ANTIBIOTICS
FILE REFERENCE: 660081.406
TITLE
                               APPLICANT:
                                                APPLICANT:
                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH:
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les 12; Conserv
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OF INVENTION:
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12; Conserv
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Taylor, Robert
Erfle, Douglas
Fraser, Janet R.
West, Michael H.P.
MCNICOl, Patticia J.
MCNICOL, COMPOSITIONS F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FastSEQ for Windows Version 3.0
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Erfle, Douglas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Krieger, Timothy
                                                                                            Krieger, Timothy
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nilarity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                                                                           100.0%;
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Pred. No.
                                                                                                                                                                                                                                                                                              Mismatches
     AND METHODS FOR TREATING
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8.8e-05;
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; OTHER INFORMATION: Cationic Peptide Analogue
US-09-030-619-107
Search completed: January 15, 2003, 18:13:20 Job time : 11 secs
                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Cationic Peptide Analogue US-09-030-619-109
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US-09-030-619-109
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SEQ ID NO 109
LENGTH: 13
TYPE: PRT
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TITLE OF INVENTION: WITH ANTIBIOTICS
FILE REPERBNCE: 660081.406
CURRENT APPLICATION NUMBER: US/09/030,619B
CURRENT FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 232
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                  Query Match
Best Local S
Matches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 109, Application US/09030619B Patent No. US20020035061A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 35.7%; Score 86; DB 10; Best Local Similarity 41.9%; Pred. No. 9.5e-05; Matches 13; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Taylor, Robert
APPLICANT: Erfle, Douglas
APPLICANT: Erfle, Douglas
APPLICANT: Fraser, Janet R.
APPLICANT: West, Michael H.P.
APPLICANT: West, Michael H.P.
APPLICANT: MCNICOL, Patricia J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
TITLE OF INVENTION: WITH ANTIBIOTICS
FILE REFERENCE: 660081.406
CURRENT FILING DATE: 1998-02-25
CURRENT FILING DATE: 1998-02-25
CURRENT FILING DATE: 1998-02-25
COURRENT FILING DATE: 1998-02-25
                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                      Local Similarity
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                                                                                WWPWRRKHEAEPEAEPIMILKKWPWWPWRRK 37
                                                                                                                                                                                                                                                                                                                                                                                               FastSEQ for Windows Version 3.0
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                                                                                                                                                                  Conservative
                                                                                                                                                                                    35.7%; Score 86; DB 10; 100.0%; Pred. No. 9.5e-05;
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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1: /cgn2_6/ptodata/1

2: /cgn2_6/ptodata/1

3: /cgn2_6/ptodata/1

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5: /cgn2_6/ptodata/1

6: /cgn2_6/ptodata/1
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77.761 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compu
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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US-08-915-314-69
US-08-915-314-45
US-08-915-314-45
US-08-915-314-45
US-08-915-314-45
US-08-915-314-38
US-08-915-314-45
US-08-915-314-38
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Sequence 54,
Sequence 55,
Sequence 55,
Sequence 62,
Sequence 63,
Sequence 64,
Sequence 36,
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38, Appl
56, Appl
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62, Appl
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US-09-099-631A-12
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79	80	80	80	81	82	82	82	82	82.5	83	83	83	83	83	83	83	83.5
32.8	33.2	33.2	33.2	33.6	34.0	34.0	34.0	34.0	34.2	34.4	34.4	34.4	34.4	34.4	34.4	34.4	34.6
17	16	15	14	11	13	13	13	13	21	20	13	13	13	13	13	12	15
4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4
US-08-702-054B-42	US-08-702-054B-2	US-08-702-054B-41	US-08-702-054B-18	US-08-915-314-75	US-08-702-054B-33	US-08-915-314-67	US-08-915-314-66	US-08-915-314-25	US-08-915-314-48	US-08-915-314-47	US-08-702-054B-35	US-08-702-054B-31	US-08-702-054B-30	US-08-915-314-50	US-08-915-314-49	US-08-915-314-24	US-08-702-054B-39
	Sequence 2	Sequence 4	Sequence 1	Sequence 7	Sequence 3	Sequence 6	Sequence 6	Sequence 2	Sequence 4		Sequence 3	Sequence 3	Sequence 3	 Sequence 5 	Sequence 4	Sequence 2	Sequence 3
	2, Appli	41, Appl	•	75, Appl	•	•	•	25, Appl	•	•	•	•	•	•	`	`	39, Appl

ALIGNMENTS

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PATENT NO. 6191254

PATENT NO. 6191254

GENERAL INFORMATION:
APPLICANT: Falls, Timothy J.
APPLICANT: Hancock, Robert E. W.
APPLICANT: Gough, Monisha
TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES
TITLE OF INVENTION: AND METHODS OF SCREENING FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-099-631A-12
                                                                                                                                                                                                                                                                                                                                       US-08-702-054B-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity ba...
Conservative
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CURRENT FILING DATE: 1998-06-18
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENCTH: 63
TYPE: PRT
                                                                                                                                                                                                                                                                                                    Sequence 38, Application US/08702054B Patent No. 6191254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Selsted, Michael E.
APPLICANT: Osapay, Klara
TITLE OF INVENTION: Crosslink-Stabilized Indolicidin Analogs
FILE REFERENCE: P-UC 3050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence FEATURE:
COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                        STREET: """
CITY: La Jolla
CTATE: CA
TSA
                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, St
                                                    STATE: C
                                                                                                                                                                                                                                                                                                                                                                                                                 11 KWPWWPWRRM-----ARIAMILPWKWPWWPWRR 38
                                                                                                                                                                                                                                                                                                                                                                                                                                    4 KWPWWPWRRKHEAEPEAEPIMILK-KWPWWPWRR 36
                                      92037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55.4%;
64.7%;
                                                                                                             Square, Suite 1400
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Pred. No. 2.9e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63;
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US-08-915-314-54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO:
                                TELEFAX: (206) 682-6031
[NFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURENT APPLICATION DATA:
APPLICATION UNMBER: US/08/915,314 FILING DATE: 20-AUG-1997 CLASSIFICATION: 424 ATTORNEY/AGENT INFORMATION: NAME: NO. 6180604tenburg Ph.D., Carol REGISTRATION NUMBER: 39.317
                                                                                   REFERENCE/DOCKET NUMBER: 66
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/002,6
FILING DATE: 23-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING TITLE OF INVENTION: INFECTIONS USING ANALOGUES OF INDOLICIDIN NUMBER OF SEQUENCES: 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
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LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/002,687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Taylor, Robert APPLICANT: Erfle, Douglas
                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
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                   LENGTH:
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amino acid
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                   21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Krieger, Timothy J.
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SYSTEM: Windows 95
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43.2%;
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Pred. No. 1.2e-06;
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RESULT 5
US-08-915-314-55
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US-08-915-314-56
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Sequence 55, Application US/08915314
Patent No. 6180604
GENERAL INFORMATION:
APPLICANT: Fraser, Janet R.
APPLICANT: West, Michael H.P.
                                                                                                                                                                                                               Query Match
Best Local Similarity
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APPLICANT: Fraser, Janet R.
APPLICANT: West, Michael H.P.
APPLICANT: Krieger, Timothy J
                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 56:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,314
FILLING DATE: 20-AUG-1997
                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
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TELECOMMUNICATION INFORMATION:
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NAME: No. 6180604tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
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STATE:
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nes 18; Conserv
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                                                                                                                                     ILKKWPWWPWRR-----IMILKK 18
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Taylor, Robert
Erfle, Douglas
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64.38;
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Pred. No.
                                                                                                                                                                                                               Score 98; I
                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                 DB 4;
2.5e-06;
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Best Local :
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Patent No. 6180604
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                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 66
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC competible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ATTORNEY/AGENT INFORMATION:
NAME: No. 6180604tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
               SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                     TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING TITLE OF INVENTION: INFECTIONS USING ANALOGUES OF INDOLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
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                                                                                                                                     COUNTRY:
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 APPLICATION NUMBER:
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                                                                                                                     98104
                                                                                                                                                                   Seattle
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17; Conservative
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                                                                                                                                   Washington
7: USA
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                                                                                                                                                                                 E: SEED and BERRY LLP 6300 Columbia Center,
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                                                                                                                                                                                                                                                                                                                                        West, Michael H.P.
                                                                                                                                                                                                                                                                                                                                                        Fraser,
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Taylor, Robert
Erfle, Douglas
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Erfle, Douglas
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                                                                                                                                                                                                                                                                                                                                                          Janet
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US/08/915,314
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Pred. No. 8.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                     701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 20;
                                                                                                                                                                                                                                                     INDOLICIDIN
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JS-08-915-314-62
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Best Local S
Matches 13
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                        TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/915,314
FILING DATE: 20-AUG-1997
CLASSIFICATION: 4.24
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6180604 tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 660081.405
                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: West, Michael H.P.
APPLICANT: Krieger, Timothy J.
APPLICANT: Taylor, Robert
APPLICANT: Taylor, Robert
APPLICANT: Erfle, Douglas
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING ANALOGUES OF INDOLICIDIN
                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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TELECOMMUNICATION INFORMATION:
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NAME: No. 6180604tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
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ADDRESSEE: SEED and BERRY LLP
                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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TYPE: a
                OTHER INFORMATION:
                              NAME/KEY: Modified-site LOCATION: 1
                                                                                    TOPOLOGY:
                                                                                                         STRANDEDNESS:
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                                                                                                                                         LENGTH:
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13; Conserv
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                                                                                                                                         13 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37.8%; Score 91; 100.0%; Pred. No.
             /note= "D-Form of Isoleucine"
                                                                                                                                                                                                                                                                                                                                                                                             Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center, 701 Fifth Avenue
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Length 13;

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US-08-915-314-63
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                                                                  US-08-915-314-64
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                                                                                 RESULT 9
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Sequence 64, Application US/08915314
Patent No. 5180604
GENERAL INFORMATION:
APPLICANT: Fraser, Janet R.
                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING TITLE OF INVENTION: INFECTIONS USING ANALOGUES OF INDOLICIDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/915,314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: No. 6180604tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
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LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
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COUNTRY:
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                                                                                                                                                                                                                                                                           LOCATION: 13
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                         NAME/KEY:
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                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                            linear
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100.0%;
                                                                                                                                                                                                             100.0%;
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                                                                                                                                                                                                                                                                             /note= "D-Form of Lysine"
                                                                                                                                                                                                                                                                                                                                                                                                                           63:
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                                                                                                                                                                                                             Score 91; DB 4; I
Pred. No. 1.1e-05;
                                                                                                                                                                                                Mismatches
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US-09-042-071-36
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Best Local :
                                                                                                                                                                                                                         Patent No. 6294372
                                                                                                                                                                                                                                               Sequence 36,
                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Burian, Jan
APPLICANT: Kay, Willia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO:
                                                                           APPLICANT: Kay, William W.

TITLE OF INVENTION: REPLICATION GENES AND GENE PRODUCTS FROM
TITLE OF INVENTION: SMALL CRYPTIC PLASMIDS AND METHODS FOR CONSTRUCTING
TITLE OF INVENTION: CONTROLLED-REPLICATION PLASMID VECTORS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
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NAME: NO. 6180604tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 660081.405
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: THM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Erfle, Douglas
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING ANALOGUES OF INDOLICIDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM FC COMPUTER: OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 SOFTWARE: PATENTAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 20-AUC CLASSIFICATION: 424
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                                                 STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
es 13; Conserv
COUNTRY:
                  STATE: Washington
                                                                    ADDRESSEE:
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                                                   6300 Columbia Center,
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 USA
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Conservative (
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                                                                     SEED and BERRY LLP
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20-AUG-1997
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; Pred. No.
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                                                       701 Fifth Avenue
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COMPUTER READABLE FORM:

MEDIUM TYPE:

Floppy disk

OPERATING SYSTEM:

IBM PC compatible SYSTEM: PC-DOS/MS-DOS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 57,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 37.8%;
Best Local Similarity 100.0%;
                                      TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
APPLICANT:
                                                                         ATTORNEY/AGENT INFORMATION:
NAME: NO. 6180604tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 660081.405
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: MCMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 660
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/042,071 FILING DATE: 13-MAR-1998
                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: CÓMPOSITIONS AND METHODS FOR TREATING TITLE OF INVENTION: INFECTIONS USING ANALOGUES OF INDOLICIDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Fraser, Janet R.
APPLICANT: West, Michael H.P.
APPLICANT: Krieger, Timothy J.
APPLICANT: Taylor, Robert
APPLICANT: Erfle, Douglas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                           APPLICATION NUMBER: US/08/915,314 FILING DATE: 20-AUG-1997 CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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Pred. No.
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1.1e-05;
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; STRANDEDNESS: ; TOPOLOGY: 11 US-08-915-314-57
RESULT 13
US-08-915-314-46
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US-08-702-054B-40
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Best Local Similarity
Matches 13; Conserv
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                                                                                                                                Matches
                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/702.05
FILING DATE: 23-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/002,687
FILING DATE: 23-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Lisa A.
REGISTRATION NUMBER: 38.347
REGISTRATION NUMBER: 38.347
                                                                                                                                                                                                                                                                                               TELEFAX: 619/678-5099 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Falls, Timothy J. APPLICANT: Hancock, Robert E. W. APPLICANT: Gough, Monisha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                           TELEPHONE: 619/678-5099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: La Jolla
STATE: CA
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ZIP: 92037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Fish & Richardson P.C. STREET: 4225 Executive Square, Suite 1400
                                                                1 ILKKWPWWPWRR-----
                                                                                  1 ILKKWPWWPWRRKHEAEPEAEPIMILKKWPWW 32
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                                                                                                                                             36.9%;
43.8%;
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Pred. No.
                                                                                                                                             Score 89; DB 4;
Pred. No. 2.4e-05;
                                                                                                                              Mismatches
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. 1.2e-05;
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Sequence 46, Application US/08915314
Patent No. 6180604
GENERAL INFORMATION:

APPLICANT:

Fraser, Janet R. West, Michael H.P.

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INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDJUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/915,314
FILING DATE: 20-AUG-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6180604tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 660081.405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING TITLE OF INVENTION: INFECTIONS USING ANALOGUES OF INDOLICIDIN NUMBER OF SEQUENCES: 90
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           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                           APPLICANT: Fraser, Janet R.
APPLICANT: West, Michael H.P.
APPLICANT: Krieger, Timothy J.
APPLICANT: Taylor, Robert
APPLICANT: Terfle, Douglas
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING ANALOGUES OF INDOLICIDIN
NUMBER OF SEQUENCES: 90
                                                                                                            COMPUTER READABLE FORM:
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                                                                                                                                                                   STREET: 6300 Cocity: Seattle STATE: Washing:
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                                                                                                                                 ZIP: 98104
                                                                                                                                           COUNTRY:
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Taylor, Robert
Erfle, Douglas
                                                                                                                                                                                                        6300 Columbia Center, 701 Fifth Avenue
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US/08/915,314
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RESULT 15
US-08-915-314-74
Sequence 74, Application US/08915314
Patent No. 6180604
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US-08-915-314-52
                                                                       US-08-915-314-74
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Matches
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MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PatentID Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,314
FILING DATE: 20-AUG-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 6180604tenburg Ph.D., Carol
RECISTRATION NUMBER: 39,317
REPERENCE/DOCKET NUMBER: 660081.405
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
THETERY. (206) 627-4900
Query Match
Best Local S
Matches 12
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                                                                                                                                                                                  TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Fraser,
APPLICANT: West, Mi
APPLICANT: Krieger,
APPLICANT: Taylor,
APPLICANT: Erfle, D
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ATTORNEY/AGENT INFORMATION:
NAME: No. 6180604 tenburg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING TITLE OF INVENTION: IMPECTIONS USING ANALOGUES OF INDOLICIDIN
                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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STREET: vv.
STREET: vv.
STREET: vv.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 LKKWPWWPWRRK 13
                                                                                            TOPOLOGY:
                                                                                                           STRANDEDNESS:
                                                                                                                                             LENGTH:
l Similarity
12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98104
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                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6300 Columbia Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fraser, Janet R.
West, Michael H.P.
                                                                                                                                              12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Krieger, Timothy J.
Taylor, Robert
Erfle, Douglas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (206) 622-4900
                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36.1%;
 35.7%; Score 86; DB 4; L
100.0%; Pred. No. 4.5e-05;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 87; DB 4; L
Pred. No. 3.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 12;
                                       Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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Conservative

Indels

0;

Gaps

0

Qy 1 ILKKWPWWPWRR 12
Db 1 ILKKWPWWPWRR 12
Search completed: January 15, 2003, 18:10:13
Job time: 14 secs

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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compu

Compugen Ltd

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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OM protein - protein search, using sw model
                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq
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length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    908470 segs, 133250620 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A_Geneseq_101002:*
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Listing first 45 summaries
                                                                                                                                                                                                                                                  : /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1986 DAT: *
:/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1986 DAT: *
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/SIDS2/gcgdatta/geneseq/geneseqp-embl/AA1981.DAT:*
/SIDS2/gcgdatta/geneseq/geneseqp-embl/AA1982.DAT:*
/SIDS2/gcgdatta/geneseq/geneseqp-embl/AA1983.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*
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140.865 Million cell updates/sec
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                                                              SUMMARIES
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Indolicidin analog	AAY24570	19	20	38.8	93.5	10
Amino acid sequenc	AAY91808	21	21	40.7	86	9
Indolicidin analog	AAY24571	19	21	40.7	98	œ
Amino acid sequenc	AAY91806	21	21	41.1	99	7
Indolicidin analog	AAY24582	19	21	41.1	99	6
Antimicrobial cati	AAW12899	18	16	41.3	99.5	5
Indolicidin fusion	AAY57142	21	63	55.4	133.5	4
Poly-(Indol (1-13)	AAY44668	21	63	55.4	133.5	ω
Indolicidin analog	AAW66363	19	27	57.1	137.5	2
Amino acid sequenc	AAY91800	21	28	58.7	141.5	1
Description	ID	DB	Query Match Length DB	Query Match	Score	Result

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11
85	85	85	85.5	86	86	86	86	86	86	86	86	86	86	87	87	7	87.5	7	89	91	91	91	91	91	91	91	91	91	91	91	91	91	91	93.5
35.3	٠	•	35.5	•	35.7	35.7	35.7	35.7	35.7	35.7	•		•			•	-		36.9	•	•	•		•	•	•	•	•	•	•				8
13	12	12	16	14	14	13	13	13	13	13	12	12	12	12	12	21	21	21	15	14	14	13	13	13	13	13	13	13	13	13	13	13	13	20
18	21	19	18	21	19	21	21	19	19	18	21	19	18	21	19	21	19	19	18	21	19	23	21	21	21	21	21	21	21	19	19	19	18	21
AAW27179	AAY91828	AAY24586	AAW12882	AAY91813	AAY24573	AAY91812	AAY91803	AAY24572	AAY24613	AAW12896	AAY91833	AAY24615	AAW12877	AAY91804	AAY24580	AAY91796	AAW66376	AAY24552	AAW13802	AAY91811	AAY24583	ABB81254	AAY91820	AAY91819 ,	AAY91818	AAY91774	AAY91773	AAY92795	AAY94495	AAW71690	AAW66378	AAY24609	AAW12873	AAY91807
	ശ	Indolicidin analog	Antimicrobial cati	Amino acid sequenc	Indolicidin analog		Amino acid sequenc		Indolicidin analog	ía	Amino acid sequenc	Indolicidin analog	Antimicrobial cati	Amino acid sequenc	icidi	Amino acid sequenc	Cationic peptide o	Indolicidin analog	Antimicrobial cati	Amino acid sequenc	icid	_	acid	acid	acid	acid	cid:		œ	peptide	Cationic peptide o	Indolicidin analog	Antimicrobial cati	Amino acid sequenc

ALIGNMENTS

RESULT 1 AAY91800 06-JUN-2000 (first entry) AAY91800; AAY91800 standard; Peptide; 28 AA. Amino acid sequence of cationic peptide MBI 11B20CN

Cationic peptide; tumour; pharmaceutical composition; cancer; treatment; leukaemia; polyoxyalkylene-modified; APO; lymphoma; multiple myeloma; breast; lung; ovary; cervix; uterus; skin; prostate; liver; colon; multidrug resistance.

Synthetic

NO9965506-A2

23-DEC-1999.

14-JUN-1999; 99WO-CA00552.

12-JUN-1998; 98US-0096541.

(MICR-) MICROLOGIX BIOTECH INC.

Friedland HD, Krieger TJ, Taylor R, Erfle D,

Fraser JR,

West MHP;

WPI; 2000-223549/19.

Novel pharmaceutical composition containing optionally activated polyoxyalkylene-modified cationic peptides, useful for treating tumours

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RESULT 2
AAW66363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QΥ
В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents a cationic peptide amino acid sequence, which can be used in the pharmaceutical composition of the invention. The invention relates to a pharmaceutical composition containing at least one activated polyoxyalkylene (APO)-modified cationic peptide. The modification of peptides with APO increases their activity against tumour ceils, including those with a multidrug resistant phenotype. The pharmaceutical composition can be used to treat tumours, specifically lymphoma, leukaemia, multiple myeloma, or tumours of breast, lung, ovary, cervix, uterus, skin, prostate, liver and colon.
                                                                                                                                                                                                                                                                                       25-FEB-1998;
10-MAR-1997;
20-AUG-1997;
26-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1;
                                    The present sequence represents an indolicidin analogue. The present invention describes compositions and methods for treating infection, especially bacterial infections. The compositions and methods use cationic peptides in combination with an antibiotic agent which are then administered to a patient to enhance the activity of the antibiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                               New indolicidin peptide analogues - useful for, e.g. enhancing activity of antibiotic or overcoming tolerance, acquired resistance or inherent resistance of microorganisms
                                                                                                                                                                                                                                                                                                                                                                                     17-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW66363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW66363 standard;
 peptides
                            agent,
                                                                                                                        Claim 1; Page 91; 105pp; English.
                                                                                                                                                                                                        WPI; 1998-520800/44
                                                                                                                                                                                                                                                            (MICR-) MICROLOGIX
                                                                                                                                                                                                                                                                                                                                                          10-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                              WO9840401-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indolicidin analogue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indolicidin
               inherent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RWPWWPWRRK - - -
                                                                                                                                                                                                                                   JR,
              to overcome: (a) tolerance; (b) acquired resistance; and (c) at resistance. The combinations of antibiotics and cationic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page
 can provide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fungus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28 AA;
                                                                                                                                                                                                                                   McNicol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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97US-0040649.
97US-0915314.
97US-0060099.
                                                                                                                                                                                                                                                                                                                                                           98WO-CA00190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                parasite; virus
                                                                                                                                                                                                                                                               BIOTECH INC.
                                                                                                                                                                                                                                    .
PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.7%;
58.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; resistance; cationic peptide; antibiotic;
tolerance; antibacterial; microorganism;
  synergistic activity against a microorganism that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MBI 11B20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----ILMRWPWWPWRRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English.
                                                                                                                                                                                                                                    West MHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 141.5;
Pred. No. 3.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .6e-11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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RESULT 3
AAY44668
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                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is tolerant, inherently resistant, antibiotic agent. They can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                       protozoacide; virucide; anti-HIV; human immunodeficiency virus-1;
HIV-1; gram positive bacteria; gram negative; Staphylococcus aureus;
Escherichia coli; Salmonella typhimurium; yeast; fung1; protozoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Crosslinked indolicidin analog; X-indolicidin; poly-Indol 1-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY44668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY44668 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  parasites and viruses.
                                                                                                                                                                                                                                                                   Cleavage-site
                                                                                                                                                                                                                                                                                      Cleavage-site
                                                                                                                                                                                                                                                                                                           Cleavage-site
                                                                                                                                                                                                                                                                                                                               Cleavage-site
                                                                                                                                                                                                                                                                                                                                                    Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                    Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              stability; bovine neutrophil; anti
protozoacide; virucide; anti-HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Poly-(Indol (1-13)-Met-Ala-Arg-Ile-Ala-Met)3 protein.
                                                                                                                                                                                                    Region
                                                                                                                                                                                                                         Cleavage-site
                                                                                                                                                                                                                                              Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                                                                                       Bos sp.
                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                     hexapeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Candida albicans;
WPI; 2000-147133/13
                      Selsted ME,
                                       (REGC ) UNIV
                                                               18-JUN-1998;
                                                                                                                           WO9965510-A1
                                                                                                                                                          Region
                                                                                                                                                                               Region
                                                                                   20-MAY-1999;
                                                                                                       23-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 RWPWWPWRRK-----MIL-RWPWWPWRRK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KWPWWPWRRKHEAEPEAEPIMILKKWPWWPWRRK 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     spacer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                     Osapay K;
                                          CALIFORNIA
                                                              98US-0099631
                                                                                   99WO-US11165
                                                                                                                                                                                                                          /label=
58..59
                                                                                                                                                                                                                                                                    /label=
39..40
                                                                                                                                                           /label=
58..63
                                                                                                                                                                                                                                                                                        /label=
25..26
                                                                                                                                                                                 /label=
39..44
                                                                                                                                                                                                                                                44..45
                                                                                                                                                                                                     /label=
20..25
                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                          /label=
                                                                                                                                                                                                                                                                                                                                                               /label=
                                                                                                                                                                                                                                                        /label=
                                                                                                                                                                                                                                                                                                                     /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cryptococcus neoformans; Giardia; Acanthamoeba;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.1%;
61.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             y resistant, or has acquired resistance can be used for killing e.g. bacteria,
                                                                                                                                                                                                                                    Cyanogen_bromide_cleavage_site
                                                                                                                                                                                                                                                         Cyanogen_bromide_cleavage_site
                                                                                                                                                                                                                                                                             Cyanogen_bromide_cleavage_site
                                                                                                                                                                                                                                                                                                 Cyanogen_bromide_cleavage_site
                                                                                                                                                                                                                                                                                                                                           Enterokinase_cleavage_site
                                                                                                                                                                                                                                                                                                                                                               Enterokinase_recognition_site
                                                                                                                                                                                                               Cyanogen_bromide_cleavage_site
                                                                                                                                                                                                                                                                                                                      Cyanogen_bromide_cleavage_site
                                                                                                                                                Hexapeptide_spacer
                                                                                                                                                                     Hexapeptide_spacer
                                                                                                                                                                                          Hexapeptide_spacer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 137.5; DB 1
Pred. No. 1.1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antimicrobial; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fungicide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fungi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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RESULT 4
AAY57142
   CCC XXX PTT TID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (X'indolicidin) analogs are stable and have antimicrobial activity against gram positive and negative bacteria (e.g. Staphylococcus aureu Escherichia coli and Salmonella typhimurium), yeasts and fungi (e.g. Candida albicans, Cryptcocccus neoformans), protozoa (e.g. Giardia species and Acanthamoeba species), and viruses (e.g. HIV-1). They can be used for reducing or inhibiting the growth or survival of microorganisms in an environment e.g. a food or food product, a solution, an inanimate object comprising a surface, or a mammal. The present sequence is a protein comprising three copies of Indol 1-13 each separated by a hexapeptide spacer sequence. A recombinant construct encoding this sequence was used for the expression of Indol-homoserine (Hse) analog. The ability of Indol-Hse analog to maintain antimicrobial activity provides a means tenderical activity provides a means tenderical activity provides and the construction antimicrobial activity provides and the sequence was used for the supersection of Indol-homoserine (Hse) analog. The ability of Indol-Hse analog to maintain antimicrobial activity provides a means the provides and the sequence was used for the sequence was used for the sequence.
                                     Disclosure; Fig 6; 62pp; English
                                                                  New indolicidin analogues, active against bacteria, yeast, protozoa and virus, used for, e.g. treating infections - \,
                                                                                                                          WPI; 2000-053028/04.
N-PSDB; AAZ45123.
                                                                                                                                                                                                                                                                                                                                                               WO9958141-A1
                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indolicidin analogue; antimicrobial activity; helminth; bacteria;
treatment; inhibit growth; micro-organism; contact lens solution;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY57142 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The patent discloses crosslinked analogs of indolicidin (Indol 1-13) which is a naturally occurring peptide isolated from bovine neutrophils and has antimicrobial activity. The crosslinked indolicidin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Crosslinked indolicidin analogs with antimicrobial activity against bacteria, yeast, fungi, protozoa and viruses
                                                                                                                                                                                  Selsted
                                                                                                                                                                                                                                                         12-MAY-1998;
                                                                                                                                                                                                                                                                                            05-MAY-1999;
                                                                                                                                                                                                                                                                                                                               18-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                    transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indolicidin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY57142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1C; Fig 1; 53pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAZ49764
                                                                                                                                                                                                                    (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 KWPWWPWRRKHEAEPEAEPIMILK-KWPWWPWRR 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KWPWWPWRRM-----ARIAMILPWKWPWWPWRR 38
 the amino acid sequence of an example of a fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-indolicidin analog precursors in sufficient quantities.
                                                                                                                                                                                                                                                                                                                                                                                                                                inhibit growth; plant; surgical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                       98US-0076227
                                                                                                                                                                                                                                                                                            99WO-US09942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55.4%;
64.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                  micro-organism;
instrument; yeas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 133.5; DB Pred. No. 9e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                  yeast; fungi; protozoa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
protein which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ç
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RESULT 5
AAW12899
Дb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xaa9 = at least one amino acid;
provided that if Xaa1 is present, Xaa8 = Hse, Met or Met-Xaa9-Met;
and further provided that: if Xaa2 is absent, Xaa1 is absent; if Xaa3 is
absent, Xaa1 and Xaa2 are absent; if Xaa4 is absent, Xaa1, Xaa2 and Xaa3
are absent; and if Xaa5 is absent, Xaa1, Xaa2, Xaa3 and Xaa4 are absent.
The indolicidin analogues can be used to create a fusion polypeptide
consisting of the analogue linked to a peptide. The indolicidin
analogues have antimicrobial activity against gram positive bacteria,
gram negative bacteria, yeast, fungus, protozoa and viruses (e.g. HIV-1).
They are also active against helminths. The analogues can be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    reducing or inhibiting growth or survival of a microorganism. They can be used for treating infections. They can also be included in a liquid such as water or an aqueous solution, e.g. contact lens solution. The analogues have potential uses in food products, and in objects such as the surface of an instrument used to prepare food or to perform surgery. Transgenic plants or animals useful in the food industry can be produced by introducing a nucleic acid molecule encoding an indolicidin analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xaa4 = Xaa5 = Xaa6 = Xaa7 = Xaa8 = Xaa9 = Xa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xaa2 =
Xaa3 =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          consists of an indolicidin analogue linked to another peptide. Peptides AAY57109-Y57138 and AAY57143-Y57144 are new indolicidin analogues, which have a homoserine residue and/or a truncated amino terminal region. The analogues have the following amino acid sequence:
                       Falla TJ,
                                                                         (UYBR-) UNIV BRITISH COLUMBIA
                                                                                                                                                                                         23-AUG-1996;
                                                                                                                                                                                                                                                 06-MAR-1997.
                                                                                                                                                                                                                                                                                                      W09708199-A2
                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                      Shigella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bacterium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antimicrobial cationic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW12899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW12899 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Where:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xaal-Xaa2-Xaa3-Xaa4-Xaa5-Xaa6-Pro-Xaa6-Yaa6-Pro-Xaa6-Xaa7-Xaa7-Xaa8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  into the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 KWPWWPWRRM-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 KWPWWPWRRKHEAEPEAEPIMILK-KWPWWPWRR 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trp, Phe or absent;
Arg, Lys or absent;
Trp or Phe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ile, Leu, Val, Ala, Gly
Ile, Leu, Val, Ala, Gly
Pro or absent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l Similarity
22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        homoserine (Hse), Met, Met-Xaa9-Met or absent, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               germline cells of such organisms.
                    Gough M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        viral; antitumour; food; preservative; inhibitor; growth;
yeast; endotoxaemia; sepsis; antibiotic; fungal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                    95us-0002687
                                                                                                                                                                                         96WO-IB00996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    albicans; sterilant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -ARIAMILPWKWPWWPWRR 38
                       Hancock REW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 133.5; DB Pred. No. 9e-10; O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or absent; or absent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CP-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
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2

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RESULT 6
AAY24582
ID AAY2
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DRXX PARKET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a specifically claimed novel isolated CC cationic peptide which has antimicrobial activity. The amino acid CC sequence of antimicrobial cationic peptides (including the present CC sequence) is selected from: XIXIPTOXXXXXPTO(XXXPTO)XXX3(X5)o; CC XIXIPTOXXXXX4(X5)PTOXXXXXX; XIXIPTOXXXXXPTO(XXXPTO)XXX3(X5)o; CC XIXIXXXXXXPTO(XXXPTO)XX2(X5)m; where m = 1-5; n = 1-2; o = 2-5; r CC = 0-8; u = 0-1; X1 = Ile, Leu, Val, phe, Tyr, Trp or Met; X2 = Trp or CC Pro. The peptides are preferably amidated or carboxymethylated. The CC peptides may be used in methods for inhibiting the growth of a bacterium CC or yeast, or for inhibiting an endotoxaemia or sepsis associated CC disorder in a subject. The peptides have a broad activity against the CC antibiotic resistant bacteria, combined with activity against the CC medically important fungus Candida albicans. In addition, the peptides CC may be used as sterilants or preservatives of materials susceptible to CC microbial or viral contamination, e.g. in processed foods to inhibit CC salmonella, Yersina and Shigella. The peptides are compact and tend to CC have a unique polyproline type II extended helix structure that permits consistent than permits the membrane with relatively few amino acids. The peptides consoled the ability to work synergistically with antibictics, and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cationic peptide(s) having anti-microbial activity - used for the inhibition of bacterial and viral growth, as an antitumour agent,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-179179/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY24582 standard; peptide;
WPI; 1998-169090/15
                                                                                                13-JAN-1997;
21-AUG-1996;
                                                                                                                                                                                                                                                                       additive; shampoo; soap;
food; technical material
                               Erfle D,
                                                             (MICR-) MICROLOGIX BIOTECH INC
                                                                                                                                              21-AUG-1997;
                                                                                                                                                                            26-FEB-1998
                                                                                                                                                                                                             WO9807745-A2
                                                                                                                                                                                                                                                                                                       antimicrobial; antibiotic; antiarrythmic;
                                                                                                                                                                                                                                                                                                                       Indolicidin;
                                                                                                                                                                                                                                                                                                                                                    Indolicidin analogue #34.
                                                                                                                                                                                                                                                                                                                                                                                      18-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ب
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ILKKWPWWPWRRKHEAEPEAEPIMILKKWPWWPWRRK 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as a food preservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          some of then possess anti-endotoxin activity.
                                 Fraser JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 AA;
                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                      bacterial infection; photo-oxidised solubiliser;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66;
                                                                                                97US-0034949.
96US-0024754.
                                                                                                                                              97WO-US14779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41.3%;
                               Krieger TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English.
                                                                                                                                                                                                                                                                                         insecticide; herbicide; preservative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 99.5; D
Pred. No. 3.7e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -WPWWPWRRK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.5;
No. 3
                               Taylor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 18;
3.7e-06;
                                                                                                                                                                                                                                                                                                       surface disinfectant;
                                 Ħ
                                  West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                  MH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
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WPI; 2000-223549/19 Friedland HD, (MICR-) MICROLOGIX BIOTECH INC

98US-0096541. 99WO-CA00552

Krieger TJ,

Taylor

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Erfle

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Fraser

JR,

West MHP;

14-JUN-1999;

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RESULT 7
AAY91806
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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY24549 to AAY24615 represent indolicidin analogues of formulae (I)-(VIII) containing up to 25 amino acids (aa): RXXXXXB (I), BXXXXXXB (II), BXXXXXXBB (II), BXXXXXXBB (II), BXXXXXXBB (AA), MMLBBAGS (IV), BXXXXXXBB (AA), MMLBBAGS (IV), BXXXXXXBB (AA), MMLBBAGS (IV), BXXXXXXBB (AA), MMLBAGS (IV), BXXXXXXBB (AA), MMLBAGS (IV), BXXXXXXBB (AII), WHERE Z = P OT V; X = hydrophobic residue, preferably W; B = basic aa, preferably R OT K; AA = any aa; n = 0 OT 1; in (II), at least 1 Z = V; in (VIII) at least 2 X = F OT Y. The analogues are used to treat infections caused by bacteria (Gram positive or negative, or anaerobic); fungi (yeast or moulds); parasites (protozoa, nematodes, cestodes or trematodes) or viruses. Typical of very many pathogens that can be controlled are Leishmania, Trypanosoma, Ascaris lumbricoides, Fasciola becontrolled are Leishmania, Trypanosoma, Ascaris lumbricoides, Fasciola becontrolled are Leishmania, Engletchella pertussis. Stabbulococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 materials. The analogues are administered by injection, lavage, orally or topically, generally at 0.1-50 mg/kg. These analogues have a broader spectrum of activity than indolicidin and modification as compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hepatica, Klebsiella pneumoniae, Bordetella pertussis, Staphylococcus aureus, Listeria, Clostridium, rotavirus and papilloma virus. Compounds derived from the analogues may be used similarly; the compounds may also be prepared from antibiotics or antiarrythmic agents. The analogues may be used therapeutically or to coat medical devices; also they are useful as surface disinfectants, as additives to shampoo or soaps, as insecticides or herbicides, or as preservatives for foods and technical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 13; Page 89; 129pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid - vectors, transformed cells and antibodies, conjugates with polyoxyalkylene glycol and fatty acid to rtoxicity, useful therapeutically, as disinfectants etc.
                                                                                                                                                                                                                                                                                                                                     Cationic peptide; tumour; pharmaceutical composition; cancer; treatment; leukaemia; polyoxyalkylene-modified; APO; lymphoma; multiple myeloma; breast; lung; ovary; cervix; uterus; skin; prostate; liver; colon; multidrug resistance.
                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY91806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY91806 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New indolicidin analogues with antimicrobial activity and related
                                                                                                                                                                                                                                                              W09965506-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                          Amino acid sequence of cationic peptide MBI 11D4CN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                reduces their toxicity.
                                                                                                                                                                                                                         23-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ILKKWPWWPWRRK------MILKK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ILKKWPWWPWRRKHEAEPEAEPIMILKK 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41.1%;
64.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 99;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .9e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
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RESULT 8
AAY24571
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cells, including those with APO increases their activity against tumour pharmaceutical composition can be used to treat tumours, specifically lymphoma, leukaemia, multiple myeloma, or tumours of breast, lung, ovary, cervix, uterus, skin, prostate, liver and colon.

Sequence 21 AA.
AAY24549 to AAY24615 represent indolicidin analogues of formula (I)-(VIII) containing up to 25 amino acids (aa): RXZXXZXB (I), (II), BBBXZXXZXB (III), BXZXXZXBR (III), BXZXXZXBRR (VI), BXZXXZXBXB (VI), LBBNXZXXZXRK (VI), LKNXZXXZXRKK (VII) and BBXZXXZXBBB Where Z = p or V; x = hydrophobic residue, preferably W; B = ba preferably R or K; AA = any aa; n = 0 or 1; in (II), at least 1 in (VIII) at least 2 x = f or Y. The analogues are used to trea
                                                                                                        Claim
                                                                                                                           New indolicidin analogues with antimicrobial activity and nucleic acid - vectors, transformed cells and antibodies, conjugates with polyoxyalkylene glycol and fatty acid to toxicity, useful therapeutically, as disinfectants etc.
                                                                                                                                                                                                                                                                        13-JAN-1997;
21-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel pharmaceutical composition containing optionally activated polyoxyalkylene-modified cationic peptides, useful for treating tumours
                                                                                                                                                                                               WPI; 1998-169090/15
                                                                                                                                                                                                                                                                                                              21-AUG-1997;
                                                                                                                                                                                                                                                                                                                                         26-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                  WO9807745-A2
                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                               additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                           antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY24571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY24571 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 15;
                                                                                                                                                                                                                                                (MICR-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indolicidin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indolicidin analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                   tood;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ILKKWPWWPWRRKHEAEPEAEPIMILKK 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence
                                                                                                        12;
                                                                                                                                                                                                                                                                                                                                                                                                                   technical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        equence represents a cationic peptide amino acid sequence, used in the pharmaceutical composition of the invention.
                                                                                                                                                                                                                                                MICROLOGIX BIOTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                               shampoo;
                                                                                                      Page 89; 129pp;
                                                                                                                                                                                                                       Fraser JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          bacterial infection; photo-oxidised solubiliser;
1; antibiotic; antiarrythmic; surface disinfectant;
ampoo; soap; insecticide; herbicide; preservative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                        97US-0034949.
96US-0024754.
                                                                                                                                                                                                                                                                                                             97WO-US14779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41.1%;
64.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94pp;
                                                                                                                                                                                                                       Krieger
                                                                                                      English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -MILKK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 99;
Pred. No.
                                                                                                                                                                                                                       ΤJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                     Taylor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .9e-06;
                                                                                                                                                                                                                     ₽,
                                                                                                                                                                   activity and
                                                                                                                                                                                                                       West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                  XB (I), BXZXXZXB
BXZXXZXBB(AA)nM
                                                                             formulae
                                                                                                                                           reduce
                                                                                                                                                                   related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
              basic a
t 1 Z =
                                       (VIII).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
               : aa,
= V;
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fungi (yeast or moulds); parasites (protozoa, nematodes, cestodes or trematodes) or viruses. Typical of very many pathogens that can be controlled are Leishmania, Trypanosoma, Ascaris lumbricoides, Fasciola hepatica, Klebsiella pneumoniae, Bordetella pertussis, Staphylococcus aureus, Listeria, Clostridium, rotavirus and papilloma virus. Compounds derived from the analogues may be used similarly; the compounds may also be prepared from antibiotics or antiarrythmic agents. The analogues may be used therapeutically or to coat medical devices; also they are useful as surface disinfectants, as additives to shampoo or soaps, as insecticides or herbicides, or as preservatives for foods and technical materials. The analogues are administered by injection, lavage, orally or topically, generally at 0.1-50 mg/kg. These analogues have a broader spectrum of activity than indolicidin and modification as compounds
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        infections caused by bacteria (Gram positive or negative,
                                                                                                           their
AA;
                                                                                                     toxicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        anaerobic);
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Q
g
                             Matches
                                           Query Match
                                     Local
1 ILKKWPWWPWRRKHEAEPEAEPIMILKK
                             18;
                                     Similarity
                             Conservative
                                    40.7%;
64.3%;
-IMILKK
                             0;
                                    Score 98; I
Pred. No. 7.
                             Mismatches
              28
                                           DΒ
                                    .8e-06;
                             0;
                                          Length
                             Indels
                             10;
                            Gaps
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1;

RESULT 9
AAY918008
ID AAY9
XX AAY9
AC AAY9
XX AAY1
DE Amin
XX Cati
KW Leuk
KW Leuk
KW Mrea
KW mult
XX W099
XX W099
XX W099
XX W12-\
YX W11-\
YX W11-\
YX WPI
XX WPI
XX WPI
XX WPI
XX WPI
XX WPI
XX Thi
CC Can
CC Lym
CC Cel
CC Cer Amino acid sequence of cationic AAY91808; AAY91808 standard; (first entry) Peptide; 21 A peptide MBI 11D6CN

multidrug resistance leukaemia; po breast; lung; Cationic peptide; tumour; pharmaceutical composition; cancer; treatment; polyoxyalkylene-modified; ng; ovary; cervix; uterus; APO; i lymphoma; multiple myeloma; prostate; colon;

Synthetic

14-JUN-1999; 99WO-CA00552

(MICR-) MICROLOGIX BIOTECH INC.

12-JUN-1998;

98US-0096541

HD Krieger TJ, Taylor R, Erfle 'n Fraser JR, West MHP;

WPI; 2000-223549/19

polyoxyalkylene-modified Novel pharmaceutical composition cationic containing optionally c peptides, useful for treating tumours activated

Disclosure; Page 15; 94pp; English.

This sequence represents a cationic peptide amino acid sequence, which can be used in the pharmaceutical composition of the invention. The invention relates to a pharmaceutical composition containing at least one activated polyoxyalkylene (APO)-modified cationic peptide. The modification of peptides with APO increases their activity against tumour cells, including those with a multidrug resistant phenotype. The pharmaceutical composition can be used to treat tumours, specifically lymphoma, leukaemia, multiple myeloma, or tumours of breast, lung, ovary, approximate the composition of the composit uterus, colon

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RESULT 10
AAY24570
Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H
                                                                                      CA AAY24549 to AAY24615 represent indolicidin analogues of formulae CC (I)-(VIII) containing up to 25 amino acids (aa): RXZXXXB (I). BXZXXZXB (III). RXZXXZXB (III). BBBXZXXZXB (III). BXZXXZXB (III). RXZXXZXB (VI). EXZXXZXBBR (AA)nMILBBAGS (IV). BXZXXZXBB (VIII). CC (V). EXZXXZXXB (VI). EXZXXXXRRK (VII) and BXZXXXXXBB (VIII). CC (VIII). At least 2 X = F or Y. The analogues are used to treat (CC infections caused by bacteria (Gram positive or negative, or anaerobic): CC infections caused by bacteria (Gram positive or negative, or anaerobic): CC (infections caused by bacteria (Gram positive or negative, or anaerobic): CC (infections caused by bacteria (Gram positive or negative, or anaerobic): CC (infections caused by bacteria (Gram positive or negative, or anaerobic): CC (infections caused by bacteria (Gram positive or nematodes, cestodes or CC (controlled are Leishmania, Typical of very many pathogens that can be hepatica, Klebsiella pneumoniae, Bordetella pertussis, Staphylococcus (CC causeus, Listeria, Clostridium, rotavirus and papilloma virus. Compounds (CC also be prepared from antibiotics or antiarrythmic agents. The analogues (CC also be prepared from antibiotics or antiarrythmic agents. The analogues (CC also be used therapeutically or to coat medical devices; also they are useful as surface disinfectants, as additives to shampoo or soaps, as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indolicidin; bacterial infection; photo-oxidised solubiliser;
antimicrobial; antibiotic; antiarrythmic; surface disinfectant;
additive; shampoo; soap; insecticide; herbicide; preservative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New indolicidin analogues with antimicrobial activity and related nucleic acid - vectors, transformed cells and antibodies, also conjugates with polyoxyalkylene glycol and fatty acid to reduce toxicity, useful therapeutically, as disinfectants etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indolicidin
                 insecticides or herbicides, or as preservatives for foods and technical materials. The analogues are administered by injection, lavage, orally or topically, generally at 0.1-50 mg/kg. These analogues have a broader spectrum of activity than indolicidin and modification as compounds
                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 12; Page 89; 129pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-169090/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MICR-) MICROLOGIX BIOTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-FEB-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ILKKWPWWPWRR-----IMILKK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ILKKWPWWPWRRKHEAEPEAEPIMILKK 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ive; shampoo; soap;
technical material.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity
18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fraser JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           analogue #22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,
     toxicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-0034949.
96US-0024754.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97WO-US14779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40.7%;
64.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Krieger TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 98;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Taylor R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 21;
7.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          West MH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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RESULT 11
AAY91807
ID AAY91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SX
XX
                                                                                                    PF
CIG
밁
                       Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 17; Conser
                                                   Matches
                                                              Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY91807 standard; Peptide; 20
                                                                                                                                                                  This sequence represents a cationic peptide amino acid sequence, which can be used in the pharmaceutical composition of the invention. The invention relates to a pharmaceutical composition containing at least one activated polyoxyalkylene (APO)—modified cationic peptide. The modification of peptides with APO increases their activity against tumour cells, including those with a multidrig resistant phenotype. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9965506-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             multidrug resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           breast; lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cationic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY91807;
                                                                                                                             cells, including those with a multidrug resistant phenotype. The pharmaceutical composition can be used to treat tumours, specifically lymphoma, leukaemia, multiple myeloma, or tumours of breast, lung, overervix, uterus, skin, prostate, liver and colon.
                                                                                                                                                                                                                                                                                              Novel pharmaceutical composition containing polyoxyalkylene-modified cationic peptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                             14-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cationic peptide; tumour; pharmaceutical composition; cancer; treatme leukaemia; polyoxyalkylene-modified; APO; lymphoma; multiple myeloma; breast; lung; ovary; cervix; uterus; skin; prostate; liver; colon;
                                                                                                    Sequence
                                                                                                                                                                                                                                                          Disclosure; Page 15; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                   12-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                       (MICR-) MICROLOGIX BIOTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ₩
             1 ILKKWPWWPWRRKHEAEPEAEPIMILKK 28
\vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ILKKWPWWPWRR------MILKK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ILKKWPWWPWRRKHEAEPEAEPIMILKK 28
                                                                                                                                                                                                                                                                                                                                        2000-223549/19.
                                                  l Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                HU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence of cationic peptide MBI 11D5CN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
                                                                                                      20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA;
                                                                                                                                                                                                                                                                                                                                                                Krieger TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0096541
                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-CA00552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38.8%;
                                                                38.8%;
60.7%;
                                                                                                                                                                                                                                                                                                                                                                  Taylor R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
  MILKK 17
                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 93.5; DB 19 Pred. No. 2.7e-05;
                                                                Score 93.5;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AΑ
                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                  Erfle D,
                                                                 .7e-05;
                                                                             DB
                                                                                                                                                                                                                                                                                                   poptionally useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19;
                                                                               21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                       0,
                                                                                                                                                                                                                                                                                                                                                                   Fraser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                               Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer; treatment;
                                                                                                                                                                                                                                                                                                    activated treating tumours
                                                                                                                                                                                                                                                                                                                                                                    JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
                                                       11;
                                                                                                                                                                                                                                                                                                                                                                    West MHP;
                                                                                                                                               lung, ovary,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                       Gaps
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RESULT 12 AAW12873 ID AAW12

AAW12873 standard; peptide;

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RESULT 13
AAY24609
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                                                                                                                               Query Match
Best Local (
                                                               Matches
                                                                                                         N.B. The present sequence represents SEQ ID NO:1 in the claims and examples of the specification, but differs slightly from the SEQ I in the sequence listing on page 51 of the specification (see AAW27 \,
                                                                                                                                                                                                                                                                                            The present sequence represents a specifically claimed cationic peptide which has antimicrobial activity. The
                                                                                                                                                                                                                                                                                                                                   Cationic peptide(s) having anti-microbial activity - used for the inhibition of bacterial and viral growth, as an antitumour agent, and as a food preservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacterial; viral; antitumour; food; preservative; inhibitor; bacterium; yeast; endotoxaemia; sepsis; antibiotic; fungal; antiviral; Candida albicans; sterilant; Salmonella; Yersina;
                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-179179/16
                                                                                                                                                                                                                                                                                                                                                                                    Falla
                                                                                                                                                                                                                                                                                                                                                                                                                  23-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                 23-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W09708199-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shigella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antimicrobial cationic peptide CP-11
                                                                                                                                                                                                                                                                                                                                                                                                   (UYBR-) UNIV BRITISH COLUMBIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-DEC-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW12873;
                                _
                                              Н
                             ILKKWPWWPWRRK 13
                                                                                                                                                                                                                                                                                                                    2; Page 65; 89pp; English.
                                                                     Similarity
                                                                                             13
                                                                                                                                                                                                                                                                                                                                                                                   Gough M,
                                                              Conservative
                                                                                             A
                                                                                                                                                                                                                                                                                                                                                                                                                 9505-0002687
                                                                                                                                                                                                                                                                                                                                                                                                                                96WO-IB00996
                                                                     37.8%;
100.0%
                                                                                                                                                                                                                                                                                                                                                                                   Hancock REW;
                                                                     .08;
                                                              0
                                                                     Score 91;
Pred. No.
                                                              Mismatches
                                                                     DB 18;
3.5e-05;
                                                                           Length 13
                                                             Indels
                                                                                                                                                                                                                                                                                                    novel
                                                             0;
                                                                                                           AAW27179).
                                                                                                                                                                                                                                                                                                    isolated
                                                            Gaps
                                                                                                                   ID NO:1
                                                            0;
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δÃ
                                                                                                                                                                   CC (A)-(VIII) containing up to 25 amino acids (aa): RXZXXZXB (I), BEXXXZXB (III), BEXXXXZXB (III), BEXXXXZXB (III), BEXXXXXB (III), BEXXXXXB (III), BEXXXXXB (A), MMCC (III), BEXXXXXXB (VII), BEXXXXXBB (AA), MMCC (V), LBBNXXXXXXKK (VI), LKNXXXXXKK (VII) and BEXXXXXXBBB (VIII).

CC Where Z = P or V; X = hydrophobic residue, preferably W; B = basic aa, preferably R or K; AA = any aa; n = 0 or 1; in (II), at least 1 Z = V; in (VIII) at least 2 X = F or Y. The analogues are used to treat (I) in (VIII) at least 2 X = F or Y. The analogues are used to treat (I) in (VIII) at least 2 X = F or Y. The analogues are used to treat (I) in (VIII) at least 1 Z = V; in (VIII) at least 2 X = F or Y. The analogues are used to treat (I) in (VIII) at least 1 Z = V; in (VIII) at least 2 X = F or Y. The analogues are used to treat (I) in (VIII) at least 1 Z = V; in (VIII) at least 2 X = F or Y. The analogues are used to treat (I) at least 2 X = F or Y. The analogues and pathogens that can be controlled are Leishmania, Trypanosoma, Ascaris lumbricoides, Fasciola (I) in (VIII) at least 1 A Typanosoma, Ascaris lumbricoides, Fasciola (I) in (VIII) at least 1 A Typanosoma, Ascaris lumbricoides, Fasciola (I) in (VIII) at least 2 X = F or Y. The analogues may be used similarly; the compounds may compounds from analogues may be used similarly; the compounds may also be prepared from antibiotics or antitarrythmic agents. The analogues are constitutes to shampoo or soaps, as insecticides or herbicides, or as preservatives for foods and technical constants. The analogues are administered by injection, lavage, orally constants that I in the individual and modification as compounds or spectrum of activity than indolicidin and modification as compounds or spectrum of activity than indolicidin and modification as compounds or spectrum of activity than indolicidin and modification as compounds
                                                                                   Matches
                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New indolicidin analogues with antimicrobial activity and related nucleic acid - vectors, transformed cells and antibodies, also conjugates with polyoxyalkylene glycol and fatty acid to reduce toxicity, useful therapeutically, as disinfectants etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indolicidin; bacterial infection; photo-oxidised solubiliser; antimicrobial; antibiotic; antiarrythmic; surface disinfectant; additive; shampoo; soap; insecticide; herbicide; preservative; food; technical material.
                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-169090/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Erfle D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-JAN-1997;
21-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9807745-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY24609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 32; 129pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY24609 standard; peptide; 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MICR-) MICROLOGIX BIOTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indolicidin analogue #61.
1 ILKKWPWWPWRRK
                                         1 ILKKWPWWPWRRK
                                                                                                      Similarity
                                                                                                                                                                                                         their toxicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fraser JR,
                                                                                                                                                                   13
                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97US-0034949
96US-0024754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97WO-US14779
                                                                                                    37.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Krieger TJ,
                                                                                   0
                                                                                                    Score 91;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA.
                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Taylor
                                                                                                    3.5e-05;
                                                                                                                        DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    æ
                                                                                                                          19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    West
                                                                                                                      Length 13;
                                                                                Indels
                                                                              0;
                                                                              Gaps
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RESULT 14 AAW66378

Вb

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AAW71690
ID AAW7
XX
AC AAW7
AC AAW7
DT 11-J
XX
DE Cati
XX
KW MBI1
KW repl
                                                                                                                                                                                                                          DЬ
                                                                                                                                                                                                                                                      QΥ
                                                                                                                                                                             RESULT 15
                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-FEB-1998;
10-MAR-1997;
20-AUG-1997;
26-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a specifically claimed cationic peptide from the present invention. The present invention describes compositions and methods for treating infection, especially bacterial infections. The compositions and methods use cationic peptides in combination with an antibiotic agent which are then administered to a patient to enhance the activity of the antibiotic agent, to overcome: (a) tolerance; (b) activity of the antibiotic agent, to overcome: (b) tolerance; (c) inherent resistance. The combinations of antibiotics and cationic peptides can provide synergistic activity against a microorganism that is tolerant, inherently resistant, or has acquired resistance to an antibiotic agent. They can be used for killing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cationic peptide of claim 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW66378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New indolicidin peptide analogues - useful for, e.g. enhancing activity of antibiotic or overcoming tolerance, acquired resistance or inherent resistance of microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9840401-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bacteria; fungus; parasite; virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW66378 standard; peptide; 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indolicidin analogue; resistance; cationic peptide; antibiotic;
bacterial infection; tolerance; antibacterial; microorganism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-520800/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fraser JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MICR-) MICROLOGIX BIOTECH INC.
              MBI11; cationic peptide; plasmid pKL1; small cryptic plasmid; replication; RepA; vector; RAMP.
                                                                                                                                                                                                                                                                                                                                             Sequence
                                                         Cationic peptide MBI11 (MW 1879).
                                                                                                                                                 AAW71690 standard; Peptide; 13 AA
                                                                                        11-JAN-1999
                                                                                                                     AAW71690;
                                                                                                                                                                                                                                                                                                                                                                        .g. bacteria, fungi, parasites and viruses.
                                                                                                                                                                                                                          1 ILKKWPWWPWRRK 13
                                                                                                                                                                                                                                                        1 ILKKWPWWPWRRK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 93; 105pp; English
                                                                                                                                                                                                                                                                                                                                               13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          McNicol
                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0030619.
97US-0040649.
97US-0915314.
97US-0060099.
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100.0%; Pred. No. 3.5e-05;
Nismatches 0;
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Search completed: January 15, 2003, 18:08:34 Job time: 36 secs

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Best Local S
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                                                                                                                                     MBIII is a small (mol.wt. 1879) cationic peptide. DNA encoding MBIII has been incorporated into vector pp21-BI, in which the replication leader (R21) sequence of RepA (see also AAW71686) is joined to 2 Hpro peptides (see also AAW71692), to provide a vector for expression of MBIII in host cells. The invention provides controlled replication plasmid vectors (RAMP vectors) comprising a replication origin of a small cryptic plasmid and a gene encoding RepA. The vectors can reach very high levels of plasmid replication, but are not lethal to the host cell, and can be used to direct the high level expression of e.g. cytokines, antigens and therapeutic proteins.
                                                                                                                                                                                                                                                                                                                                           Increasing plasmid copy number in a cell with the repA gene product - and an small cryptic plasmid ori sequence, useful for high level expression of e.g. cytokines, antigens or therapeutic proteins
                                                                                                                                                                                                                                                                                                                                                                                                                               Burian J, Kay WW;
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             1 ILKKWPWWPWRRK 13
1 ILKKWPWWPWRRK 13
                                                ch 37.8%;
l Similarity 100.0%;
l3; Conservative (
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Title:
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                               US-09-444-281-35-27-35
241
1 ILKKWPWWPWRRKHEAEPEAEPIMILKKWPWWPWRRK 37
                                                                                                                                                                                                                                                           GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb:
6: sp_manmal:*
7: sp_mhc:*
8: sp_organel1
9: sp_phage:* 10: 11: 12: 13: 14: 15: 16: sp_archea:*
sp_bacteria:*
sp_fungi:* sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:* sp_mammal:*
sp_mhc:* sp_organelle:* sp_invertebrate:* sp_rodent:*
sp_virus:* sp_plant:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

Qy Db	DR DR SQ	DR RT T	AÇ TETTTOOOO SOOOOX SOOO	RESULT Q9Y7V5 ID Q
QUELY MATCH 29.0%; PEROL NO. 2.3; Best Local Similarity 29.0%; Pred. No. 2.3; Matches 9; Conservative 2; Mismatches 9; Indels 11; Gaps 1; 4 KWPWWPWRRKHEAEPEAEPIMILKKWPWWPW 34 1	; Claudin. ; S_mold_repeat. ; S_mold_repeat; 2. LAUDIN; UNKNOWN_1. 135824 MW; 3249C749AFAOCDF8	[1] SEQUENCE FROM N.A. STRAIN-ATCC 32173; MEDLINE-99343881; PubMed-10413618; Puyesky M., Benhamou N., Ponce Noyola P., Bauw G., Ziv T., Van Montagu M., Herrera Estrella A., Horwitz B.A.; "Developmental regulation of cmpl, a gene encoding a multidomain Conidiospore surface protein of Trichoderma."; Fungal Genet. Biol. 27:88-99(1999). EMBL; AJ133651; CAB40845.1; HSSP: P01180; NPPO.	09Y7V5; 01-NOV-1999 (TrEMBLrel. 12, Created) 01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Conidiospore surface protein. CMP1. Trichoderma harzianum. Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; mitosporic Hypocreales; Trichoderma. MCBL_TaxID=5544;	LT 1 V5 Q9Y7V5 PRELIMINARY; PRT; 1245 AA.

34.4%;

Pred. No.

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Best Local Similarity 33...
Matches 11; Conservative
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Q9DUC4;
01-MAR-2001
01-MAR-2001
01-JUN-2002
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TT virus.
                                                                                                                                            MEDLINE=20534983; PubMed=11080484;
Okamoto H., Nishizawa T., Tawara A., Peng Y., Takahashi M.,
Kishimoto J., Tanaka T., Miyakawa Y., Mayumi M.;
"Species-specific TT viruses in humans and nonhuman primate
phylogenetic relatedness.";
Virology 277:368-378(2000);
Virology 277:368-378(2000);
EMBL; AB041959; BAB19313.1;
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01-OCT-2000
01-OCT-2000
01-JUN-2002
                                              SEQUENCE
                                                              Pfam; PF02956; TT_ORF1; 1.
PROSITE; PS00131; CARBOXYPEPT_SER_SER; UNKNOWN_1
                                                                                                                                                                                                                                                                                         STRAIN-MF-TTV9;
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SEQUENCE
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"The entire nucleotide sequences of two distinct isolates (TJN01 and TJN02) remotely related to isolates.";
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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InterPro; IPR004219; TTvirus_Unk.
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MEDLINE=20456801; PubMed=11003468;
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AB028669; BAA94878.1; -.
PEO: IPR004219; TTVITUS_Unk.
PEO:2956; TT_ORF1; 1.
NCE 746 AA; 88561 MW; E01
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Matches
                                                                                                                                                                                                                              Q9DT80;
Q9DT80;
01-MAR-2001
01-MAR-2001
                                                                        EMBL; AB050449; BAB19930.1; -. NON_TER 49 49 5EQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q91RD8;
01-DEC-2001
01-DEC-2001
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                                                                                                                            Okamoto H., Nishizawa
Sai T., Sugai Y.;
                                                                                                                                               MEDLINE=20568739;
                                                                                                                                                      STRAIN-TYM9
                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                           Viruses;
                                                                                                                                                                                                                     01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                          Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases EMBL; AF371370; AAK54733.1; -. InterPro; IPR004219; TTVINS_UNk. Pfam; PF02956; TT_ORF1; 1. SEQUENCE 175 AA; 22073 MW; 5212D7DA3FD72F81 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORF3
                                                                                                           "TT virus mRNAs detected in the bone marrow cells individual.";
                                                                                                                                                                                  NCBI_TaxID=68887;
                                                                                                                                                                                                   TT virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-LO3;
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nes 11; Conserv
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WTWW-WQRRRRR-
                  WPWWPWRRKHEAEPEAEPIMILKKWPWWPWRRK 37
                                                                                                                                                                                                             (Fragment).
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                                    l Similarity
10; Conser
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                                                                       49 AA; 7225 MW;
                                     Conservative
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                                                                                                                                    PubMed=11118348;
zawa T., Tawara A.,
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                                            26.1%;
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Last sequence up
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Last annotation updat
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Pred. No. 0.
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2; Mismatches
                                                                      1DA6F8F1AB69AA43 CRC64
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Pred. No. 2.1;
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-WPWRRR 19
                                    Mismatches
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Viruses;
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Q9Z8B7;
01-MAY-1999
MEDLINE-20568739; PubMed-11118348;
Okamoto H., Nishizawa T., Tawara A
Sai T., Sugai Y.;
"TT virus mRNAs detected in the bo
                                                                                                                 ORF1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99206606; PubMed=10192388; Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.; "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CT277 SIMILARITY (CPJ0426 protein).
CPN0426 OR CPJ0426 OR CP0327.
Chlamydia pneumoniae (Chlamydophila pneumoniae)
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydo
                                                                                                                                      01-MAR-2001
01-MAR-2001
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Eisen J., Fraser C.M.;
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                                                        SEQUENCE FROM N.A.
                                                                               NCBI_TaxID=68887;
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(TrEMBLrel. 10, Last sequence up)
(TrEMBLrel. 19, Last annotation
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                                                                                                                                                                                                                                                                              Conservative
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21:385-389(1999).
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                                                                                          viruses;
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42.3%;
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 marrow
                      Takahashi
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K., Bass
Dodson R.
Salzberg
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       MEDLINE-87064324; PubMed-3023845; D'Ambrosio E., Waitzkin S.D., Witney F. "Structure of the highly repeated, long or LlRn) of the rat."; Mol. Cell. Biol. 6:411-424(1986). EMBL; M13100; AAA66046.1; -... InterPro; IPR000566; Lipocln_cytFABP. PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.
                                                                                                                                                   Q63778 PRELIMINARY; PR Q63778; O1-NOV-1996 (TrEMBLrel. 01, Crea 01-NOV-1996 (TrEMBLrel. 17, Last Hypothetical 43.7 KDa protein.
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TT virus.
Viruses; :
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                                                                                     TISSUE=LIVER;
                                                                                                                                   Rattus norvegicus (Rat)
Eukaryota; Metazoa; Cho
                                                                                                                                                                                                                                                                                                                                                                     multiple tissues from infect
Virology 288:358-368(2001).
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Yoshikawa A.;
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01-DEC-2001
                                                                                             SEQUENCE FROM N.A.
                                                                                                               NCBI_TaxID=10116;
                                                                                                                          Mammalia;
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Sciurognathi;
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                   SEQUENCE FROM N.A.

STRAIN=AN19 / DSM 6324 / JCM 9639;

MEDLINE=21927647; PubMed=11930014;

Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,

Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,

Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,

Malykh A.G., Koonin E.V., Kozyavkin S.A.;

"The complete genome of hyperthermophile Methanopyrus kandleri AV19

and monophyly of archaeal methanogens.";

Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
    SEQUENCE
              Complete
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SEQUENCE FROM N.A.
MEDLINE=21844401; PubMed=11855633;
Mishlzawa T., Takahashi M.,
                                                                                                                                      NCBI_TaxID=2320;
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01-MAR-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                Methanopyrus
                                                                                                                                                         Archaea;
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EMBL; AB064615; BAB79374.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TT virus.
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fam; PF02956; TT_ORF1; 1.
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les 13; Conserv
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    27799 MW;
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   B051994FE5B24E05 CRC64;
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01-MAR-2002
01-MAR-2002
                                          classifiable into the fourth viremic infants.";
Arch. Vircol. 147:21-41(2002).
EMBL; AB064598; BAB79322.1;
                                                                                                                                                                                                                                                                                                                        ORF1
InterPro; IPR004219; TTvirus_Unk. Pfam; PF02956; TT_ORF1; 1. SEQUENCE 734 AA; 86978 MW; F6
                                                                                                                              MEDLINE=21844401; PubMed=11855633; Peng Y.H., Nishizawa T., Takahashi M.,
                                                                                                                                                                                                                                                                                       TT virus.
Viruses; ssDNA viruses;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycine-rich protein LeGRP1.
Lycopersicon esculentum (Tomato).
Eukaryota; Viridiplantae; Strepto
                                                                                                 "Analysis of the complete genomes of thirteen TT virus
                                                                                                                    Okamoto H.
                                                                                                                                                             STRAIN=CT43F;
                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                      Submitted (JUL-2001)
                                                                                                                                                                                                                      Okamoto
                                                                                                                                                                                                                                   STRAIN=CT43F;
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"LeGRP1: A new member of glycine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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physiol. Plantarum 0:0-0(2001).
EMBL; AV026037; AARO8984 1; -
SEQUENCE 284 AA; 23434 MW; F
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86978 MW; F60E188BC0104A68 CRC64;
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Q98414;
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Okamoto H., Nishizawa T., Tawara A., Peng Y., T
Kishimoto J., Tanaka T., Miyakawa Y., Mayumi M.
"Species specific TT viruses in humans and nonh
phylogenetic relatedness.";
Virulogy 277:368-378 (2000)
EMBL; AB041957; BAB19308.1; -.
InterPro; IPR004219; TTvirus_Unk.
                                                                                              MEDLINE-95135990; PubMed-7834396; Woodward T.M., Carlson J.O., de la DeMartini J.C.; "Biological and genetic changes in passage in isogeneic twin lambs."; Acquir. Immune Defic. Syndr. Hun
                                                                                                                                                                                                                                                                          Ovine lentivirus.
Viruses; Retroid viruses;
NCBI_TaxID=11663;
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01-MAR-2001
Carlson J.O., Demartini J.C., Mwaengo D.M.;
"Envelope glycoprotein nucleotide sequence and genetic
                                        SEQUENCE FROM N.A.
STRAIN-85/34;
                                                                                                                                                                                                                       STRAIN-85/34
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01-JUN-2002
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                                                                                                                        in ovine lentivirus strains following
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                                                                                              8:124-133(1995).
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Вb
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                                                                                                                Query Match
Best Local
                                                                                                                                                                              characterization of North American ovine lentiviruses."; Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases. EMBL; U64439; AAB08725.1; ... InterPro; IPR000328; Env_GP41. Pfam; PF00517; GP41; 1.
                                                                                                                                                        SEQUENCE
                                                                                                                                                                    Transmembrane
223 VPYPFALLKCTKWCWYP
                                                163 ILKRVYKQDWPWNTYHWPLWQMENMRQWMKENEREYKGRTNKTKEDIDDLLAGKIRGRFC 222
                        22
                                                                                                                 Local Similarity
                                                                         1 ILKK-----WPW----WP----
                        ---PIMILK--KWPWWP 33
                                                                                                   18;
                                                                                                                                                       985 AA;
                                                                                                   Conservative
                                                                                                                                                       113794 MW;
                                                                                                                25.3%;
23.4%;
239
                                                                                                               Score 61; DB
Pred. No. 25;
                                                                                                   Mismatches
                                                                         -WRRKHEAEPEAE-
                                                                                                                                                       3197258EDBDE3597 CRC64;
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